

```

1  CCGCAACCCC GACGGCGCCC CAAACGCTGT TCGCGCGCGC GCCCCGCCCC
51  GCCCCGCCCTC GCGCTGGTCC CGGTCTCGCC CCGCAGCCCT CGATCTCCCC
101 TGACTTCCTC GGCCAGGCCG CCTGCGCCTC TGGGACCATG TTGCGCTGGC
151 TCGGGGACTT CGCGCTGCCC ACCGCGGCCT GCCAGGACGC GGAGCAGCCG
201 ACGCGCTACG AGACCCTCTT CCAGGCACTG GACCGCAATG GGGACGGAGT
251 GGTGGACATC GCGGAGCTGC AGGAGGGGCT CAGGAACCTG GGCATCCCTC
301 TGGGCCAGGA CGCCGAGGAG AAAATTTTFA CTA CTGGAGA TGTCAACAAA
351 GATGGGAAGC TGGATTTTGA AGAATTTATG AAGTACCTTA AAGACCATGA
401 GAAGAAAATG AAATTGGCAT TTAAGAGTTT AGACAAAAAT AATGATGGAA
451 AAATTGAGGC TTCAGAAATT GTCCAGTCTC TCCAGACACT GGGTCTGACT
501 ATTTCTGAAC AACAAGCAGA GTTGATTCTT CAAAGCATTG ATGTTGATGG
551 GACAATGACA GTGGACTGGA ATGAATGGAG AGACTACTTC TTATTTAATC
601 CTGTTACAGA CATTGAGGAA ATTATCCGTT TCTGGAACA TTCTACAGGA
651 ATTGACATAG GGGATAGCTT AACTATTCCA GATGAATTCA CGGAAGACGA
701 AAAAAAATCC GGACAATGGT GGAGGCAGCT TTTGGCAGGA GGCATTGCTG
751 GTGCTGTCTC TCGAACAAGC ACTGCCCTT TGGACCGTCT GAAAATCATG
801 ATGCAGGTTT ACGGTTCAAA ATCAGACAAA ATGAACATAT TTGGTGGCTT
851 TCGACAGATG GTA AAAAGAGT GAGGTATCCG CTCGCTTTGG AGGGGAAATG
901 GTACAAACGT CATCAAAATT GCTCCTGAGA CAGCTGTTAA ATTCTGGGCA
951 TATGAACAGT ACAAGAAGTT ACTTACTGAA GAAGGACAAA AAATAGGAAC
1001 ATTTGAGAGA TTTATTTCTG GTTCCATGGC TGGAGCAACT GCACAGACTT
1051 TTATATATCC AATGGAGGTT ATGAAAACCA GGCTGGCTGT AGGCAAAACT
1101 GGGCAGTACT CTGGAATATA TGATTGTGCC AAGAAGATTT TGAAACATGA
1151 AGGCTTGGGA GCTTTTACA AAGGCTATGT TCCCAATTTA TTAGGTATCA
1201 TACCTTATGC AGGCATAGAT CTTGCTGTGT ATGAGCTCTT GAAGTCCTAT
1251 TGGCTGGATA ATTTTGCAA AGATTCTGTA AACCTGGAG TCATGGTGTT
1301 GCTGGGATGC GGTGCCTTAT CCAGCACCTG TGGTCAGCTG GCCAGCTACC
1351 CATTGGCTTT GGTGAGAACT CGCATGCAGG CTCAAGCCAT GTTAGAAGGT
1401 TCCCCACAGC TGAATATGGT TGGCCTCTT CGACGAATTA TTTCAAAGA
1451 AGGAATACCA GGACTTTACA GAGGCATCAC CCCAAACTTC ATGAAGGTGC
1501 TCCCTGCTGT AGGCATCAGT TATGTGGTTT ATGAAAATAT GAAGCAAACT
1551 TTAGGAGTAA CCCAGAAATG ATGTTGCATT TTTTGCTTTA GCCTGATAAT
1601 TGAAACTTTC AACAATCTCT GGAGTGACTT TTTCTCCTCG AATTGAAACA
1651 AGTCTATGGC AAAAGAAGCT GCATTTTTTT CACAAAAGGG AAGACGGTAA
1701 CAATGGTCAC TTCAAACTTT TGGGCTAAAT TATATGTACA CAGAAATGTT
1751 CAAAATCATA GTTTTAATGT GTTTTGAAAA GGCCACACAA TTATACTTTA
1801 TCTTTTCTFA ATAATCCTGC AAATCTCTGC CCTGAATCCG AAATCTGAAA
1851 ATGTA CTGGC TTTGTTTGT GTGTTAGAGT TATAAATCAT
1901 TAATCTTTAT TTCGGGTGGT TTACGTTTAT GCCAGTTCCT TTATATTTAA
1951 ATTTCTTGTT TTATATATTT TGAATGTCTT TATAGATTTC TTTAAATTTT
2001 CTTATAGAAC CATTAAATAG AAATCATTAC ATTTAAAAATA TACCTTACAG
2051 CAAAAGCATC CAAATAAGTA TAGGGTTTAT GTCCTTATTT TTCTTTCAGC
2101 TGAATACGAA TGAACACAGT GGTGGAATTT CTGAAGGGAA GTGATGAAAT
2151 TATATTTATT TCAGTGGGCA CTTTTCCATT TTACCACTGT ACCATTATTT
2201 GGTTCTCTGA GTTATACACT AATTTTCAGT ATATTACTGT TAAATTACCA
2251 ACACAAGGCA ATTTATTTGA AAGATTCCGT TTATCCTGCC ATTGCTTTGA
2301 AAAGCAGCAG GAAACGAAAT TTTTGTACTT GTATCAGCTT CTGCAGAGCA
2351 TCTTTGTTTT CTTTGTCTT TTGTTTCTTA CCTTTTGAAT CAGATTCCGT
2401 TTTAGTCAGG AAGACTTCTT GGGACCATTC TTAGTAACCT GAAATTTCTT
2451 TTTTAATTGC ATGAAGTGGA TTGATCATGA GCAAGTGATG GGCTTTATTT
2501 CTCCCTCACT GGTGAATATC CTTTGAACCT GCTGTTTGCA ATATGGGCAG
2551 CCACAAAGGG GGAGAGATGC CTATTAAATC GGCGGGGTGT ATGACTTCTG
2601 AAAACATTGG ATACCCTATT TTGAAAAGGG AAAGGCCCAA TTTGGGGAAA
2651 CATATACCAA TGCATGATTT CTG (SEQ ID NO:1)

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FIGURE 1A

FEATURES:

5'UTR: 1-137
Start Codon: 138
Stop Codon: 1569
3'UTR: 1572

HOMOLOGOUS PROTEINS:

Top BLAST Hits:

	Score	E
CRA 335001098641184 /altid=gi 11360341 /def=pir T50686 peroxis...	927	0.0
CRA 11000479457833 /altid=gi 6841066 /def=gb AAF28888.1 AF12330...	834	0.0
CRA 18000005183605 /altid=gi 7504235 /def=pir T22688 hypotheti...	432	e-120
CRA 1000682325160 /altid=gi 7499323 /def=pir T21074 hypothetic...	377	e-103
CRA 89000000196990 /altid=gi 7294582 /def=gb AAF49922.1 (AE003...	348	9e-95
CRA 150000075553401 /altid=gi 9758252 /def=dbj BAB08751.1 (AB0...	339	5e-92
CRA 335001098657884 /altid=gi 11358611 /def=pir T49871 peroxis...	330	2e-89
CRA 163000046661776 /altid=gi 10176874 /def=dbj BAB10081.1 (AB...	326	4e-88
CRA 105000014652720 /altid=gi 10798831 /def=dbj BAB16462.1 (AP...	200	3e-50
CRA 335001098655048 /altid=gi 11277065 /def=pir T47703 Ca-depe...	199	6e-50

BLAST dbEST hits:

gi 10145202 /dataset=dbest /taxon=96...	1108	0.0
gi 1437155 /dataset=dbest /taxon=9606 ...	801	0.0
gi 10333851 /dataset=dbest /taxon=96...	745	0.0
gi 8469752 /dataset=dbest /taxon=960...	363	8e-98
gi 11684041 /dataset=dbest /taxon=96...	307	4e-81

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi|10145202 Placenta Choriocarcinoma
gi|1437155 Retina
gi|10333851 Uterus leiomyosarcoma
gi|8469752 Breast
gi|11684041 Ovary fibrotheoma

Expression information from PCR-based tissue screening panels:

Leukocyte

1 MLRWLRDFAL PTAACQDAEQ PTRYETLFOA LDRNGDGVD IGELQEGLRN
 51 LGIPLGQDAE EKIFTTGDVN KDGKLDFFEF MKYLDHEKK MKLAFKSLDK
 101 NNDGKIEASE IVQSLQTLGL TISEQQAELI LQSIDVDGTM TVDWNWRDY
 151 FLFNPVTDIE EIIRFWKHST GIDIGDSLTI PDEFTEDKK SGQWWRQLLA
 201 GGIAGAVSRT STAPLDRLKI MMQVHGSKSD KMNIFFGFRQ MVKEGGIRSL
 251 WRGNGTNVIK IAPETAVKFW AYEQYKKLLT EEGQKIGTFE RFISGSMAGA
 301 TAQTFIYPME VMKTRLAVGK TGQYSGIYDC AKKILKHEGL GAFYKGYVPN
 351 LLGIIPYAGI DLAVYELLKS YWLDNFAKDS VNPGMVLLG CGALSSTCGQ
 401 LASYPLALVR TRMQAQAMLE GSPQLNMVGL FRRIISKEGI PGLYRGITPN
 451 FMKVLPAVGI SYVYENMKQ TLGVTQK (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
 N-glycosylation site

254-257 NGTN (SEQ ID NO:7)

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE
 Protein kinase C phosphorylation site

Number of matches: 2

- 1 229-231 SDK
- 2 475-477 TQK

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE
 Casein kinase II phosphorylation site

Number of matches: 8

- 1 22-25 TRYE (SEQ ID NO:8)
- 2 65-68 TTGD (SEQ ID NO:9)
- 3 121-124 TISE (SEQ ID NO:10)
- 4 157-160 TDIE (SEQ ID NO:11)
- 5 170-173 TGID (SEQ ID NO:12)
- 6 179-182 TIPD (SEQ ID NO:13)
- 7 185-188 TEDE (SEQ ID NO:14)
- 8 227-230 SKSD (SEQ ID NO:15)

[4] PDOC00008 PS00008 MYRISTYL
 N-myristoylation site

Number of matches: 16

- 1 52-57 GIPLGQ (SEQ ID NO:16)
- 2 119-124 GLTISE (SEQ ID NO:17)
- 3 171-176 GIDIGD (SEQ ID NO:18)
- 4 201-206 GGIAGA (SEQ ID NO:19)
- 5 202-207 GIAGAV (SEQ ID NO:20)
- 6 245-250 GGIRSL (SEQ ID NO:21)
- 7 253-258 GNGTNV (SEQ ID NO:22)
- 8 283-288 GQKIGT (SEQ ID NO:23)
- 9 295-300 GSMAGA (SEQ ID NO:24)
- 10 322-327 GQYSGI (SEQ ID NO:25)
- 11 326-331 GIYDCA (SEQ ID NO:26)
- 12 359-364 GIDLAV (SEQ ID NO:27)
- 13 392-397 GALSST (SEQ ID NO:28)
- 14 399-404 GQLASY (SEQ ID NO:29)

FIGURE 2A

15 442-447 GLYRGI (SEQ ID NO:30)
 16 446-451 GITPNF (SEQ ID NO:31)

[5] PDOC00018 PS00018 EF_HAND
 EF-hand calcium-binding domain

Number of matches: 3

1 32-44 DRNGDGWVDIGEL (SEQ ID NO:32)
 2 68-80 DVNKDGKLDFFEF (SEQ ID NO:33)
 3 99-111 DKNNDGKIEASEI (SEQ ID NO:34)

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	292	312	1.053	Certain
2	345	365	0.613	Putative
3	381	401	1.544	Certain
4	446	466	0.733	Putative

BLAST Alignment to Top Hit:

>CRA|335001098641184 /altid=gi|11360341 /def=pir|T50686 peroxisomal
 Ca-dependent solute carrier [imported] - rabbit
 /org=rabbit /taxon=9986 /dataset=nraa /length=475
 Length = 475

Score = 927 bits (2371), Expect = 0.0

Identities = 454/477 (95%), Positives = 466/477 (97%), Gaps = 2/477 (0%)

Query: 1 MLRWLRDFALPTAACQDAEQPTRYETLFQALDRNGDGWVDIGELQEGLRNGLGIPLGQDAE 60
 MLRWLR F LPTAACQ AE PTRYETLFQALDRNGDGWVDI ELQEGL++LGIPLGQDAE
 Sbjct: 1 MLRWLRGFVLPTAACQGAEPTRYETLFQALDRNGDGWDIRELQEGLKSLGIPLGQDAE 60

Query: 61 EKIFTTGDVKNKGKLDFFEFMKYLDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL 120
 EKIFTTGDVKNKGKLDFFEFMKYLDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL
 Sbjct: 61 EKIFTTGDVKNKGKLDFFEFMKYLDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQTLGL 120

Query: 121 TISEQQAELILQSIDVGMTVDWNEWRDYFLFNPVTDIEETIRFWKHSTGIDIGDSLTI 180
 TISEQQAELILQSID DGMTVDWNEWRDYFLFNPV DIEETIRFWKHSTGIDIGDSLTI
 Sbjct: 121 TISEQQAELILQSIDADGMTVDWNEWRDYFLFNPVADIEETIRFWKHSTGIDIGDSLTI 180

Query: 181 PDEFTEDEKKSQWWRQLLAGGIAGAVSRTSTAPLDRLLKIMQVHGSKSDKMNIFFGGFRQ 240
 PDEFTE+E+KSGQWWRQLLAGGIAGAVSRTSTAPLDRLLK+HMQVHGSKS MNIFFGGFRQ
 Sbjct: 181 PDEFTEERKSQWWRQLLAGGIAGAVSRTSTAPLDRLLKVMQVHGSKS--MNIFFGGFRQ 238

Query: 241 MVKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKLLTEEGQKIGTFERFISGSMAGA 300
 M+KEGG+RSLWRGNGTNVIKIAPETAVKFW YEYKLLTEEGQKIGTFERFISGSMAGA
 Sbjct: 239 MIKEGGVRSWLRGNGTNVIKIAPETAVKFWVYEQYKLLTEEGQKIGTFERFISGSMAGA 298

Query: 301 TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGI 360
 TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILK+EG GAFYKGYVPNLLGIIPYAGI
 Sbjct: 299 TAQTFIYPMEVMKTRLAVGKTGQYSGIYDCAKKILKYEGFGAFYKGYVPNLLGIIPYAGI 358

Query: 361 DLAVYELLKSYWLDNFAKDSVNPVGMVLLGCGALSSTCGQLASYPLALVRTRMQAQAAMLE 420
 DLAVYELLKS+WLDNFAKDSVNPVGV+VLLGCGALSSTCGQLASYPLALVRTRMQAQAAMLE
 Sbjct: 359 DLAVYELLKSHWLDNFAKDSVNPVGLVLLGCGALSSTCGQLASYPLALVRTRMQAQAAMLE 418

FIGURE 2B

Query: 421 GSPQLNMVGLFRRISKEGIPGLYRGITPNFMKVLPAVGISYVYENMKQTLGVTQK 477. (residues 1-477 of SEQ ID NO:2)

G+PQLNMVGLFRRISKEG+PGLYRGITPNFMKVLPAVGISYVYENMKQTLGVTQK
 Sbjct: 419 GAPQLNMVGLFRRISKEGLPGLYRGITPNFMKVLPAVGISYVYENMKQTLGVTQK 475
 (SEQ ID NO:4)

>CRA|11000479457833 /altid=gi|6841066 /def=gb|AAF28888.1|AF123303_1
 (AF123303) calcium-binding transporter [Homo sapiens]
 /org=Homo sapiens /taxon=9606 /dataset=nraa /length=411
 Length = 411

Score = 834 bits (2132), Expect = 0.0
 Identities = 409/410 (99%), Positives = 409/410 (99%)

Query: 8 FALPTAACQDAEQPTRYETLFOALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTG 67
 F LPTAACQDAEQPTRYETLFOALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTG
 Sbjct: 1 FVLPTAACQDAEQPTRYETLFOALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTG 60

Query: 68 DVNKGKLDFFEFMKYLDHEKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQA 127
 DVNKGKLDFFEFMKYLDHEKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQA
 Sbjct: 61 DVNKGKLDFFEFMKYLDHEKMKLAFKSLDKNNDGKIEASEIVQSLQTLGLTISEQQA 120

Query: 128 ELILQSIDVDGTMVDWNEWRDYFLFNPVTDIEEIRFWKHSTGIDIGDSLTPDEFTD 187
 ELILQSIDVDGTMVDWNEWRDYFLFNPVTDIEEIRFWKHSTGIDIGDSLTPDEFTD
 Sbjct: 121 ELILQSIDVDGTMVDWNEWRDYFLFNPVTDIEEIRFWKHSTGIDIGDSLTPDEFTD 180

Query: 188 EKKSQWWRQLLAGGIAGAVSRTSTAPLDRLKIMQVHGSKSDKMNIFFGFRQWKEGGI 247
 EKKSQWWRQLLAGGIAGAVSRTSTAPLDRLKIMQVHGSKSDKMNIFFGFRQWKEGGI
 Sbjct: 181 EKKSQWWRQLLAGGIAGAVSRTSTAPLDRLKIMQVHGSKSDKMNIFFGFRQWKEGGI 240

Query: 248 RSLWRGNGTNVIKIAPETAVKFWAYEQYKLLTEEGQKIGTFERFISGSMAGATAQTFTY 307
 RSLWRGNGTNVIKIAPETAVKFWAYEQYKLLTEEGQKIGTFERFISGSMAGATAQTFTY
 Sbjct: 241 RSLWRGNGTNVIKIAPETAVKFWAYEQYKLLTEEGQKIGTFERFISGSMAGATAQTFTY 300

Query: 308 PMEVMKTRLAVGKTQYSGIYDCAKKILKHEGLGAFYKGYVFNLLGIIPYAGIDLAVYEL 367
 PMEVMKTRLAVGKTQYSGIYDCAKKILKHEGLGAFYKGYVFNLLGIIPYAGIDLAVYEL
 Sbjct: 301 PMEVMKTRLAVGKTQYSGIYDCAKKILKHEGLGAFYKGYVFNLLGIIPYAGIDLAVYEL 360

Query: 368 LKSYWLDNFAKDSVNPVGMVLLGCGALSSTCGQLASYPLALVRTRMQAQA 417 (residues 8-417 of
 SEQ ID NO:2)

LKSYWLDNFAKDSVNPVGMVLLGCGALSSTCGQLASYPLALVRTRMQAQA
 Sbjct: 361 LKSYWLDNFAKDSVNPVGMVLLGCGALSSTCGQLASYPLALVRTRMQAQA 410
 (SEQ ID NO:5)

Score = 80.0 bits (194), Expect = 6e-14
 Identities = 80/388 (20%), Positives = 156/388 (39%), Gaps = 59/388 (15%)

Query: 95 FKSLDKNNDGKIEASEIVQSLQTLGLTISEQQAELILQSIDV--DGTMTVDWNEWRDYFL 152
 F+LD+N DG ++ E+ + L+ LG+ ++ E I + DV DG +
 Sbjct: 21 FOALDRNGDGVVDIGELQEGLRNLGIPLGQDAEEKIFTTGDNKDGKL----- 68

Query: 153 FNPVTDIEEIRFWKHSTGIDIGDSLTPDEFTDEKKSGQWWRQLLAGGIAGAVSRTST 212
 D EE +++ K + EKK ++ L +
 Sbjct: 69 -----DFEEMKYLK-----DHEKMKLAFKSLDKNNDGKIEASEIV 105

Query: 213 APLDRLKIMQVHGSKSDKMNIFFGFRQWKEGGIRSLWRGNGTNVIKIAPETAVKFWAY 272
 L L + + ++ +I V R + N I E ++FW +
 Sbjct: 106 QSLQTLGLTISEQQAELILQSIDVDGTMVDWNEWRDYFLFNPVTDI-----EEIRFWKH 161

FIGURE 2C

Query: 273 EQYKKL-----LTEEGQKIGTFER-FISGSMAGATAQTFIYPMEVMKTRLAV-GKT 321
+ TE+ +K G + R ++G +AGA ++T P++ +K + V G
Sbjct: 162 STGIDIGDSLTIPEFTEDEKKSGQWWRQLLAGGIAGAVSRTSTAPLDRLKIMQVHGSK 221

Query: 322 GQYSGIYDCAKKILKHEGLGAFYKGYVPNLLGIIPYAGIDLAVYELLKSYWLDNFAKDSV 381
I+ +++K G+ + ++G N++ I P + YE K ++
Sbjct: 222 SDKMNIFGGFRQMKKEGGIRSLWRGNGTNVIKIAPETAVKFWAYEQYKKL-----LTEEGQ 277

Query: 382 NPGVMVLLGCGALSSTCGQLASYPLALVRTRMQAQAMLEGSPQLNMVGLFRRIISKEGIP 441
G G+++ Q YP+ +++TR+ A+ + + ++I+ EG+
Sbjct: 278 KIGTFERFISGSMAGATAQTFIYPMEVMKTRL---AVGKTGQYSGIYDCAKKILKHEGLG 334

Query: 442 GLYRGITPNFMKVLPAVGISYVYENMK 469 (residues 95-469 of SEQ ID NO:2)
Y+G PN + ++P GI VYE +K
Sbjct: 335 AFYKGYVPNLLGIIPYAGIDLAVYELLK 362 (SEQ ID NO:6)

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00153	Mitochondrial carrier proteins	305.4	3e-88	1
PF00036	EF hand	50.7	1.7e-12	3
PF00404	Dockerin domain type I	9.7	0.26	1
PF01978	Protein of unknown function	2.7	9.5	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00036	1/3	27	51	5	29	18.7	0.002
PF00404	1/1	67	85	1	22	9.7	0.26
PF00036	2/3	61	87	3	29	19.7	0.001
PF00036	3/3	90	118	1	29	17.2	0.0051
PF01978	1/1	110	121	1	13	2.7	9.5
PF00153	1/1	193	472	1	313	305.4	3e-88

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1  AACCCATGTT AGTGTGCAGT TCTGCTGGCA CACACATGCA GTTGTGTAAC
51  CACTACCACC AAAAGCAAGA TGTAATAATAG CTCCATCACC CCCACAAGCC
101 TTCTGATGCT CTTTTGTCAT CAATTCCCTT CCCGCTAGTC ACAACTGGTA
151 ACTACTGATT TGTTTTCTGT CCCTATAGTT TTGCCTTTTC CAGAATGTCA
201 TTGTTGACAG GTATCAGTAA TTCATTCCCT TTTATTGCTA ATTACTATCT
251 CACTGTATGA ATGCAACACA GGTGTGTTTAC CAGTTCACCC GTTAAAGAAC
301 ATTTTGTTC TGCGCTTGAC AGTTATGAAT AGAACTGCTA TAAACCCTCA
351 AGTAAAAGTT TTGGTGTGAA GATAATTTTC TCAGCAAAAA CGCTGACAGG
401 TAATTTTCT AAGTATTACT TTTTAAAAA AGTAAAATAG CCTGTAGCCC
451 CAGCTACTCA GGAGGCTGAG GCAGGAGAAT AGCTTGAACC CAGGAGGCGG
501 AGGTTGCAGT GAGTTGAGAT TGTGCCACTG CATTCCAGCC TGGGCGACAG
551 AGCTAGACTG TCTCAAAGAA AAAAAAAAAA AATAACAAAT AAATAAAAAAG
601 TAAAATGAAA GCATGTAAGT GTAAGATGAC TAGTTCAAGC AACCTCTCTT
651 CAAGTACAGA GTATTACAGAG TAGAGATTAA AAGAGGTTTT CAAGGACAGA
701 GAAAATTTGA AGTTTGAAGG CAGTTCCAAA GGAAGGCAAT GATTCTTAAT
751 AAGACTGGAA GTTGAAGTA ATATAAAAAAG ATAAATCAGT TTCAAGATGA
801 TTTTACTAAG CAGGCAGCCC TTAATTTACA AATTCTAGAT TCATACATAT
851 CTTAAACATA CAAAATGATA TGAGGAGAGG TAAGTTCAGG GTCTGAGTTC
901 CTGGCTGTTG TTGGAAGTGA TTTCTGTGTA GTGATTCAGA AGATGTGAGA
951 CAGCCTAATT TACAAGTACA GAGGTATCTT CTTTTCTGCA AACAGCAGTA
1001 CAACAATAGT TCCTCTTACG CAGCTGTGAA TGAACAGGAT TATTACAATT
1051 AATGATATCT CATTTGATTG GCGCCTTAGA GAATTAAGAC CTTTCACACC
1101 TAATATACAA CTTTGTGTG AAGGCAGATA TTTATATTCT CATTTTACTG
1151 ATGAGAGACT ACCCGGAGAC GCTATGTCAC ACCTGAAGGA TTAGGTACTT
1201 TCTCTGTAA GTCCAATGTT CCTCCGTTA TTCCATGCTA GGCAGTAATA
1251 AGTTCGTCT TGCCTGAGTA ATAAGCTCCA AACCTCGGAA CTGCACCCAT
1301 CTTGAGAAGG AGGAGGGCGC TGTGGTTTTT TCTGATAAGT GCAGCTGGCA
1351 GACACTCTAT ACGCTTAATC ACGGGCAAAT CCTACCTAAG CTGCCTACCA
1401 AACTAGTCTT TCTTTTCCCC GTTGCCACG CAGATGGCTG TTGATCTTTT
1451 CTGCAACAAA TCCAGGAGTT TCTCCTTTTT GTTTTATAAT TGCTCCAATA
1501 GATGCTTTAG GATTAACTC TCTGCTTTTT AAAGCAGAAT CGCCATCCCA
1551 GGTGTGCAAC CACGAAAAAA TTAGACATCC GTGAGAGACA ATGCCCTCCA
1601 TGGCCCAAGT TCCAGGCAGA GAGAAGCAGC TCTGGGCTGA CCGCCAAGGC
1651 TCCGGCCCCG GAGGGTCTTT AAGTGGAGTA ACCAGTCTTC AAGACCCCGC
1701 TCCCAAGCCA CCGACGCGCT GACGCTGCAG CCCTGGACCT GCTGGGGGCC
1751 TCTTCCTCGG ACCCGCATGC TGACAGCGGG ACTGGCAACT GGGCAGAGGT
1801 CGACCCCGGG TCCGCACAGC ACCTCCCGAG ACCCAGCTCC CAGCTCCCTC
1851 ACTTCCGGCT CTCTGGAGGC GGGCCCGGCC AGTGCCCGCG AGGCCAGCGC
1901 GCGGAGCTCC TCCCCAGCAG CGGCGGGACG GCCACACCCT GCGCGCCGCG
1951 CGGGCTCGGG TGGGGTCTCC GCTCCTGCGC CTGCGCGGCC GCAGCCGCAC
2001 CCCCAGCGGC GCCCAAACG CTGTTGCGCC GCGCGCCCCG CCCAGCCCGG
2051 CCTCGCGCTG GTCCCGTCT CGCCCCGAG CCCTCGATCT CCCGTGACTT
2101 CCTCGGCCAG GCCGCCTGCG CCTCTGGGAC CATGTTGCGC TGGCTGCGGG
2151 ACTTCGTGCT GCCCACCAGC GCCTGCCAGG ACGCGGAGCA GCCGACGCGC
2201 TACGAGACCC TCTTCCAGGC ACTGGACCGC AATGGGGACG GAGTGGTGGA
2251 CATCGGCGAG CTGCAGGAGG GGCTCAGGAA CCTGGGCATC CCTCTGGGCC
2301 AGGACGCCGA GGAGGTGGGT CGCCGCCGGG GCGCCGCTG AGCGTAGGGA
2351 GGGCTGCGGG CGCTGGGGAC ACTGCGAGGA CCGAGGAGGG CGGCGGCTTG
2401 AGGCGTTGCC AGGAGAGGAA GGAGGAACTG TGGCGCCAG CGCTCCGGTG
2451 GCTTCAGAAA CTCGGGCGTG GGGCCGCGAC CGGCGACCCC GGTAACAGAA
2501 GTGGGTCATA ATACGAAAGT CTAAGGTAT TTGTCCAGAT AAAATGAGTG
2551 TTGTGGACAC TCTGGCCAC GGGCACTGTT AAATTTTAA GAACTTTTG
2601 TCCTGAATCC ATCCCAGGTT CTTTGTTC TGTTTAATA CCTTGACAGC
2651 ATGTAATCCG TTTAGCTGT CAGACTTCAG TGGGTCCCAA GTTTGTATA
2701 AAGGCGCACA CATTGATCT CTTTGAAGC TGCTTTGTTA CAGCAGCTAT
2751 GTGTATTGTC TACTGTTTGA AAAGTGTG AAAACCAATC GCGTGTTC
2801 CCCACTTCCT GTTGAGAAGG AATGGCGGCA TTCCATTGTT TAAGACATTC
2851 CTAGGTTAAT GCCCTAGGTA CATAAATTGA TCTGAAGGTT TGACTTGACC

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FIGURE 3A

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2901 TGGCACTGAG CAATTTTCATT TTCTCTGAGT CATCTTAACT GTGCCCCCTGA
2951 ACTTCTGCCC CTTTAGTAGG GTGGAGATAT GTGGAACCTC TCCAACCCTG
3001 TTGAAGCGTT CCCTGACACT GGCATTCTCT TATCCAAAGA GGGAAAGTGA
3051 TTAGGTACT ATGAGGGCCA ACAACTGTTA TATAGTTATA TTTCATTCT
3101 CTTTTAATGT CTTTGGTAGT TATAGGCCTC TTCAGTTTAC TGTTCCTCT
3151 AGAGTCAGAT TTAGTAAGTT ACAATTTTTT TTGAAACTGC CTGTTCTGTC
3201 CAAGGTTTCAT AATACTCACC GATGATTTTA TAACACTTCT GACTGAATCT
3251 GTAGGTAGGT TCTCTATTTT ATTCTCATA TCTATCCTTT TCTCCCCCTC
3301 AATCTTGCCA AAGTTTTGTG TATTTTATTC ATACTTTGAA GGAACCAACT
3351 TTTGGTACTT TGTGCTGATT GTCCCAGAAA TGGCCAGTT GGAGTCCCC
3401 ACCATGTCCA ATCATTGGCT GGAAGCAGCC CAGGAAAGGG ACGACCTTGC
3451 TGCAGTGCAT CAGCAGATGC CAGGGTTAGA GGCTAGAGAG TGGAAGTCAA
3501 CTGTGTTCTC CACAGTAGGT GCCTTTGAAG GGAGATCTCA GTGGTACAAC
3551 TCCATGGTCC CTACAATATA CAAAAGCTCT TTGGAGTGCT CAATGATTTT
3601 TAAGATTGTA AAGGGATCCT GAGATCAAAA AGCTTGAGAA TTGCTGCTGT
3651 ATCACCATT TTAGCTAAT GCATCATATT CTGTTATATG TTTGTGTCAT
3701 AGTATATGTT ACCAATTCCT TTTAAATCAC CTTTTACTTT ATTGATAGTT
3751 TAAAAACGAT TGTAAAGTGA ATTGCAATGG ATGTCCTTTG TATTCATTTT
3801 CTCATTCTGG TTCAGTTACT JTCGTAGGAT AAATTTTGAG GAGTGGACAT
3851 TGCTGAGTCT GAAGGTAACA CACATTTTAA ACTGGGATAC GTATTGCCTT
3901 TCGGAAACCT TAGACCCATT TCACTCTTT TGA CTGACTGACAG TGCTTGCTTC
3951 TCCACATCCT CGCTCATTCA GGGTATCAGT CTTTGTAAG TCTCCTATTC
4001 TGCAGGTGAA ATTCCTTTTC ATTCCTGTC TTAGTCCATT TAGTGTGCT
4051 ATAGTGGAAT ATCTGAGACA GGGTAATTTA TAAAGAAAAG ACATTTATTT
4101 AGCTCACAGT TCCGCAGGCT GGGAGTTTAA AGAAGCGTGG TGCTGGCATC
4151 TGCTGGACTC CTGGGGAGGG CTTTCCTGCT GTGTCACAAC ATGGTGGAAG
4201 GTCAAAGTGG AAGTGGACAT GTGTGAAGAA GCAAAATCCG AGGGGTGTCC
4251 TGGCTTTATA GCAACCCAGC CTCGAGGGAA CTGATCCATT ACTGAGGGAA
4301 CTAATTCAGT CTCATGAGAG AGAGAACTCA CTCACTACTG CAAGAATGAC
4351 ACCAAGCCAT TCATGAGGGA TCTGCCTCCG TAACCCTGAC ACCTCCTGCT
4401 AAGTCCCTCC TCCCAACACG GCCACATCAG GGATCAGACT TCAACATGAG
4451 TTTTTGTGGG GACAAACAAA ACGTAGCACT TGCTTTGCCT TTTGGTTCTA
4501 TTCACATCCT CCACAGGATT GCATTATGCC TACCCATTTG GTGAGGGCAG
4551 TCTTCTTTAA TTGGTTTACT GATTCAAATG CTACCCTCCT CCAGAGACAT
4601 CCTCACAGAC ACACCCAGAA ATCATGTTTT ACCAGTTATC TGGGCATCCC
4651 TTAGTCCAGA CGAGTTGATA CATAAAATTA ACCATCACAC ATGGGATAGA
4701 ATTAGGATTA CACAGTCAAC CTTTATGGGA GAAAATTTCA GAGGCATGTC
4751 AGGGGTTTAT GTAATGTCAA GGAGTGAGGA CATTGGCTAC TTGAGCATAG
4801 AAATGAGAAC TGTGGGGTGA CTCTTCGGTG GAAAGTTTCA AGGTAGTAGT
4851 TTGTATCTAA GCCAAATACT CAGCTTGAAG CAAAATCTCT ATAAATTTTC
4901 ATCTGATTTG ATCTCATCTC CGTGTTTCCA AGCATTTGTA ATGAATTGAG
4951 CATTTAGAAG AGAACAATTT TCTGTTTAAAG TTTCTTTAGA TTTTAGATGG
5001 AAAGAATGTA GAAATAAGAG TAGAATGTAG AAATAGGTAT AAAGAATATA
5051 ATAGCTAACC ATTACTAAGT GTTCCAGAAT TATCCAGGGA AGAGAAAAGA
5101 ATTCAAGGCA AGTCCTGAGA CAAAATTAAG AACCAATTGG AAGTGAAAGC
5151 GCTACATTTT TTTTTTCTGG TATGACCTTT CTTTTCTATA TGTTCCAAAT
5201 CTCCTCACTA TGAAATTAGT GAAAAATTAA AGTTAAAAAT TAGAGAAAAT
5251 TCACATTAAG TTCTCCTAGG ACTCAGTAGT ATAAGGGTAT AGACTGAGAG
5301 TAGAATGTAG TGTGAGAACA AGGAGATACA GTATTTAACC ATTACTAATT
5351 CTCTTATACT TGTCTAGTAA TCCTATTTCC TTTTAAAAGT CTTCAGTTAT
5401 TTTCTCTTTA CGCACCTCCT TCTCCCTCTT GTCTTCTCTC TTCTACCCCC
5451 ATCTTTCTTC CTGTGGAGCC TTCATGAATG GGATTAGTGC TTGTATAAAA
5501 GTGACCTGGA AGACCTTCTC TGCCCTTCC ACCATGTGAG GACACAGTGA
5551 GAAAACAGTG GTCCATGGAA CCGGAAAGTG GGTCTCTCACT AGACAGTAAA
5601 TCTCCTAGCA CTTCTGATCTA GGACTTCCAG TGTCTGGAAC TGCAAGAAAT
5651 CAATGCTTAT TGTTTAAAGTA AGCCAGTAGT ATTTTGTGCA TAGCAGCCCA
5701 GTTGGACTAG GACAATTACC AAGAGCAAGA AGGGAAGCAG CAAGCTACAA
5751 GAGAGTTCCG TCCTTGGTGT AAATTGACCG TGTAATCCTT GTCAAGTTTG

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FIGURE 3B


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5801 AGCCTTACTG GAGCTTTACT TTCTTATTCT TAAAATGCAG ATATCTTGCC
5851 TGCATCCTGG ACAGAGCTTT TAACAAGGTC ATATGTTGCA GAATATGAAA
5901 GTTCATGTTA AAAAACCTTT TAAAATGTGG TATCCCATTT ACTAGCTGGT
5951 GAACTTCTTG AGGAACCTCT GTGCCCATGG GTATGAAGTG TATGCTGAAT
6001 GATCACCCAA TGTTAGAGGA GTGGGTGGAC TGGTAACCTG ATTTAAGGGC
6051 CATTCTAACT CTTACATTCT ATGATTTTTT TAATTCTGTC TTTAAGTTTT
6101 TACATTTACA ATCACAGAAA AAATAGTCAC ATAGAAGAAT AGTAGCTTAG
6151 CAAATGTTTA TTGCATTGAG TGGAAATCAGG ATTTCACTCC ATTAAGTAAT
6201 TCCTCTGTTA ACAAAGAGGG TTCATTTTCT TTTTATTTCA TTAATATTGC
6251 TTTTTTTTTT TTTTTTCTGG AGACAGAATC TTGCTCTATC ACCAAGGCTG
6301 GAGTGCAGTG GTGCGATCTC GGCTCACTGC AGCCTCTGCT TCCTGGATTG
6351 AAGCGATTCT TGTGCCTCAG CCTCCCAAGC AGCTGAGATT ACAGGCACAT
6401 GCCACCACAC CTGGTTAACT TTTGTATTTT CTAGTAGAGA TGGGATTTTG
6451 CCATGTTGGT CAGGCTGGTC TTGAATTCCT GGCCTCTAGT GATCTGCCTG
6501 CCTCTGCCTC TGAAAGTGCT AAGATTACAG GCATGAGCTA CCATGGCCAG
6551 CCCATTTCTT TAATATTTTA ATTGTCAGAC ATGTTATGGT TTCTGGCACA
6601 ATATTAAGAA GACATGATAT GAAATCACAG GGTGAATTTT AGGGCATCAC
6651 AACAGAAAGA TTATGGTATA AGAAAAACAA TGGAAATCCA ACTACATTTT
6701 TGTCAAATGT TCTAAAATAT ATAAAATCTG TATCTTTTGT GTTCTCTCCT
6751 GATTTATATT CTAAATTTGA TGTATCTCTT CTCTGCAGAA ATAAAGTGTC
6801 TGAAAGAATG AAAAAAATGG AAGAATTCTT TAGTAAGGTA TAAATACCCG
6851 TTTCTATCTT TGTAGCATTG TAAGCCTTTT GTCACCTTTC CAAACTCCCA
6901 ACATGCCATA TTCCCTGACT AGGCCACAGC CATGTACATT GATCCCTTTA
6951 TTTTCTTCTC TCTGCCTGAG ATTTCTCTCA TTCCCCCTTC TCTGCCTGGT
7001 ATATGATTGC CCATTGTTTA AGGCCCAAC TCACCTTTAT AATCTTCCTA
7051 GCCCACTTTC TTTATCGGTA TTCCAGAAAA AACAAAAGAA GCTTCCACAA
7101 GACAACATTC TGTAATACAC TGCTTAACTT CTTTGTACCC TGCTGAGTTC
7151 AAAAATCTTA TCTTTTAAAG GATTGAATGG AGTCCACCAA GGTATCTATA
7201 TTTGACAGGA TTTATGAAAA CAAAAGGATT TGTGAGAAA GTTTGAAGCC
7251 TAACCTGAA ACCTGGATCA TAGTGTTTAC TACACATTAA CTGTTTTAGT
7301 GGATGTAATA GTTATTATTA TAGGCTGTGG AATCAGAACA GGGTTCAAAT
7351 GTTTTCACCG CTTGCTAGAC TGTGGCCTTG GGCATGTTAT TTAATGCCTG
7401 GAGGCCTCAA ATGTTAACTA GGAATGGTAA GACCTACCCA GTAACCTAGC
7451 ATAAATAGTA AATTCATTCA TTTAATGTTT TCAAACAGTG CCAGACATTG
7501 TTTAATGAAC TGGGGATATA GTGGTGAACA ACACTGACAG CGTTCTTCAT
7551 TGTATTCTCA AAACCTCCC TATAGTAAGT AGGTCTGTGT GTGTGTGTAG
7601 GTGCATGGGG AATAAAAAAT AATAAGCAAA TAATGAACAG GGTAATTTCA
7651 AAAAGCAGAA AGAGCTATTG AACAAAACTA CCTGCCTTTT ATTAGATGAA
7701 ACTCTCAACT CTATGGTTTG TTCTCTCCTG TCAATTCTGT TAAATGCTGT
7751 CAGCCTGTTT TCCTTATCAC CCTGGCCACG ACTTCTGTCT TTTCTGCTTG
7801 GTCCTGTAGA CTCTAACCCA AGGCTCATTG TCTGCCTGGC TATCTGCCTT
7851 CTGTGGCTCT TTGCCACTAC CTACATTTTC TGTGTTGCAC AGGGAAGGAC
7901 CATTCCCTGT GGACCATAAA ATTCTCTTTT TGAAAGAATT CATTCTTGAT
7951 TGGGCCACAG CACATCTTGT GAAACAGCAT TAGACATTTG CCACTGCTCA
8001 GCAGCTCTGG GGGAAAATGT TTAGTGAGAA GCGTACAGTA GTTTTTTTGA
8051 CTAACCATGG TGCAACCTCC TCCCAGAGGG AAACCTATGA GTATTTCAAG
8101 GACATGTGAT GGTCTGTTTT TGTCCCCAGT ATCTGACATG ATGGGTAGTG
8151 TAGAGCAAGA GCTTACAGAT AATGGCTAAA TTAAATTTTC TTTTTGAATT
8201 TTAATATTCA ACTTTTTAGG GTACCCAATC TCCATATTTA GGAAAAATAA
8251 TTACATAAAA AGTGAGAGT TTTTATTGTG AAACCTGCAC TCCATATTCC
8301 CAGTGGTGCA GGATGAGGGA GCACAGGTGT TGGTCTGGGG AAGCCAGGGC
8351 CCTCTGTGGT TCTGGAGGGT GAGGATTAAG AGGAAGCCTT AGATAGTATT
8401 TATGAGTATC TGCTGACTTC TCTCTGGGAC CCAAGATCAC TGAACCTTTG
8451 CCTATTTTGA GTCATCTTTT CCAATCCAGC CACTAACAGC TGAAGGATAG
8501 GCTTGCCCTG GAGCCATTGT AGTGGTTGGA TGAAGATAAA AGATAAAAAA
8551 CTGTGAGGGG AGGTGTCACA GAAGAAAGGG CCCATGTGGG CAGATTTTCA
8601 TTCAATTCCT AGTCTTTATT ACAGCAATTC TCCAGTGCTG CAACCTTAGA
8651 AAAGGATTCC TACAACACAA TGTAGGTACC CATCAGCAGC AGATTGGATA
  
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FIGURE 3C

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8701 AAGAAAATGT GGTACATACA CACCATGGAA TACTATGCAG CCATAAAAAA
8751 GGAGCAAAAT CATGTCCTTT GCAGCAATAT GAATGCAGCT GGAAGCCAAT
8801 AACTTAAACG AATTATTGTA GAAACAGAAA AACAAATACT GTGTTCTCAT
8851 TTACAGGGGG AGCTAAACCT TGGGTAAATG GGGCATAAAG ATGGGAACAA
8901 TAGACACTAG GGACTCCAAA AGGGGGGAGG GAGGGAGGAG GGCAAGGGCT
8951 GGAAAGCTTC CTACTGGGTA CTTTGTTCAC AACCTGGGTG ATGGCACGAT
9001 TAGGAGCTCA AACCCCACTA TCACACAGTA TACCCTTGTA ACAAGCTGAT
9051 GGTGTAACCC CTGAATCTAC AATAAAATTA TTTTATTTTA AAAAATCATT
9101 ATAAGGATTT TTA AAAAGAA GGATTCTAG ACAGGTGCAG CCAAAACAATT
9151 TTTTTTAAAT GTTGGCAGGC CGCCACCGCC AGTCACTTAT GCTGCAATAG
9201 CCCATGTCCC AACATTCCCA ACCTACTTCT CTCCAAAAGA GAAGCTATAC
9251 TTTCAGATGG CCCTGTGCTG GGTCTCCCTT GGAAGTTTCT GGGGAAAGGG
9301 GCTTGAGTTG CCCCAGCTGG ACTCTTCTG GAGTGGGAGC CGGGGCTTCT
9351 GATCAGACGT GAGTGAGGCA GGAACTCCGC GGTCTCCAG CGCAGCCCAG
9401 AGTGCGGTCC CACGCAGGTC CCGGTCTCTG CGCGCTCGCG CCTTTGCGCT
9451 GAAGCCGTTA GGATGAGCCC TCTCCTTCCA GAGCTTTAAC CGATGAAGGT
9501 GCATTGTGTT TGGCGCCCTT GAGGAGGATG CTGTCTTAGG CCTCTTCCCA
9551 CTGGAGCTGT GTGGTGGGCA GAGATCCGT TCGTGCGTCG CACTTCCACC
9601 CCGCTGGGGC TCACTCAGGC CGCGGAGCTG CGAGGGAGAC ATCCTCGATG
9651 GACTCCCTCT ACGGAGATCT CTTTTGGTAC CTGGAATAA ACAAGGATGG
9701 GACCTTGGAC ATTTTGTAGC TTCAGGAAGG CCTGGAGGAT GTAGGGGCCA
9751 TTCAATCTCT AGAGGAAGCG AAGGTGGGTC TCACTGGGCG TGTAATCAGA
9801 GAGACGTTGG GGCTGGGAGC CCTGGAGAGG CATTGGGCAG AGAGGGCAAA
9851 ATTTACATGT TGTCAAGCTT GACCTGGGCC CACTGCAGTG TTCAGGTGGT
9901 TGACCAGCGT TACCGTTTAT TAAGAATAAC AACACAGCTA ACACATTTCT
9951 CAAGTATTTT TCTCCGTTT CTCTTGGCT GTAGTAAAT CTCCAACCTC
10001 AGATTGCTCT CAAGATGTTG GCTACATACA GCCTTGTCTT AGGAGTCACC
10051 TTGTTCAATG TGCTCACCTG TCATTAGTCA CCCAGAGGGG CGTCTAGGCT
10101 AAAGATGCGC CCTCCCCAGT TCAGAGAACT GGAATAATCA CTCTACGTGT
10151 ATTTGGGAGT GGGGTGGTGA TTGGAAATTT TCTGATGTTA TGTTTTGGTT
10201 TCTGTTCCTG GAGGGGGGCA GTGGAAGTGG CTTTTACTCT CGGGTTTCAC
10251 TAGTGCTGAG GTTTCCTCAT AATATGCCTT AATTGATAGA CCCTAGTTAT
10301 CAGTACCGAG CTTAGGCTAA CCCTTCTCTT CCCCAGAAGG CTAACCTACA
10351 GGCTCCTTCT CAGCATGTTG TGCTTCGTAC ATACTCCTAT TGCAGTATTT
10401 CCAAGTCATT TTTCAATTGG AATTTATTAT TGTATATAAT AATTACTTTA
10451 TAAGTATATT TGCTCTTTGG ATGTTTGACC CGGTAGACTG GGAGATCATG
10501 AGCATGTGGA CTATTGAGTT TATTTTGGAT AATTGGTACT TCGTGCCCAA
10551 AAAACTGTCA GTTGAGTTCT GTCATGTTGA AATTTAGTAA AACTCTTTCT
10601 ATTAGCCATG TGAACCTTGG GAATATTGAA GCATCCATTC AGTCATGGGT
10651 CAGTTCTAGT TTGAGCACAT TCTATATTCC AAGCCCCATA CCCTGGTATC
10701 CTCATCTGTT ATATCAGAGG CCTGGACTGT GTACTTTCTG TGGACCAATT
10751 CAGTCCAAAA TGTATTCTCT GCAAAAGCTTA TCTGGATTTT TAATTCCTAG
10801 AAAAAAGCAG TGTCTCTCCT TTTAAAGTTA AGTGTCTTTG TTCAGGTGCA
10851 GTGGCTCATG CCTGTAATTC CAGCACTTTG GGAGGCCAAG GCAGGTGGAT
10901 CACTTGGGGT CAGGAGTTCA AGACCAGCCT GGCCAATATG GTAAAACCCC
10951 ATCTCTACTA AAAATGCAAA AATTAACCGG GTGTGGTGGT GGGTGTGTGT
11001 AGTCCCAGGA GGCTGAGGCA GGAGAATCAC TTGAGCCTGG GAGGCAGAGG
11051 TTGCAGCAAG CTGAGATTGC ATCACTGCAC TCCAACCTGG GTGACAGAGT
11101 GAGACTCCAT CTCAAAAAGA AAAAAAAAAA GTTAAGTGTT CTTTATATTT
11151 GTTTAAAGAC ACTCTTATAT TTAGATTTGC AAGTGTAAGT TGTATTTGTT
11201 TATTTGATAC AAAGTAGCCT TTCATAAGAA ATTCTGGGTT AGCTATCAAG
11251 TCGAATCTTT TGAAACACAT TTCTTCCTTA TTGAAACAAA AGGTTTGTAG
11301 AGCTGTCTTG CATTTTGGGC AAGGACGCTT TGTGTACCTA GTGGTGACTG
11351 AGGAGGGTTC ACATGTCAAA ACCCAAGGGA GGGGTGTCCC CAGAGAATTC
11401 TGCACCAACC ACACAGAACA TTCTGTTTCA GAGGAGCACC ATTGTGACTT
11451 TTCCTCAAGT GGCAGTCACA TCGTTAGGAG GTTTTGATGT GAGGTCTCTT
11501 CCCACACGTC TCCACCTCCC CAGTAGGAAA ATTTGTTTAT ATAGACAAAA
11551 CTCAACTGAT TAAAAAATA AAAAAAGAAAT GATACTTACA TTGTCGTGTT

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FIGURE 3D

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11601 AAGATACAAA AGCAATAACT TTTTATTGTG AAAATAGTCT GTTTTTGAAC
11651 AATATATTGT TTTGTTTTTT CCTGTGAAAG TTGAGAACT AAATATACGA
11701 AGAGATAATG GTCAGACCAT AAATAAAAAT AGAACTTTGA CTCAAATTT
11751 ACAGCAGTCT GCCCAGAAAA CCAGCCCTTT ATCTAAAATA AACAGACCAG
11801 GAAACCAGCC TGTTATGTCA GACTTATAGG AAGTCAGGTT GCTATCTCTA
11851 GAGACAATAC ACAAAGCTAT GCAATAACTG CTGTAACAGC CCCAAATGGT
11901 CAGAATTTGA TTAATAACCG ACAGCCCCCC TAATTTTTTT CTTCACNNNN
11951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNTT
12001 ACCGCTTGCT AGAACTGTGG CCTTGGGTCA TGTTATTTAA TGCCTGGAGG
12051 CCTCAAATGT TAACTAGGTA ATGGTAAGAC CTACCCAGTA ACTTAGCATA
12101 AATAGTAAAT TCATTCAATT AATGTTTTCA AACAGTGCCA GACATTGTTT
12151 AATGAACTGG GGATATAGTG GTGAACAACA CTGACAGCGT TCTTCATTGT
12201 ATTCTCAAAA CCTCCCTAT AGTAAGTAGG TCTGTGTGTG TGTGTAGGTG
12251 CATGGGGAAT AAAAAATAAT AAGCAAATAA TGAACAATAA AATTATTTTA
12301 TTTAAAAAAA AAGAAATGAT ACTTACATTG TCGTGTTAAG ATACAAAAGC
12351 AATAACTTTT TATTGTGAAA ATAGTCTGTT TTTGAACAAT ATATTGTTTT
12401 GTTTTTCTCT GTGAAAGTTG AGAACTAAA TATACGAAGA GATAATGGTC
12451 AGACCATAAA TAAAAATAGA ACTTTGACTC AAAATTTACA GCAGTCTGCC
12501 CAGAAAACCA GCCCTTTATC TAAAAATAAC AGACCAGGAA ACCAGCCTGT
12551 TATGTCAGAC TTATAGGAAG TCAGGTTGCT ATCTCTAGAG ACAATACACA
12601 AAGCTATGCA ATAAGTCTG TAACAGCCCC AAATGGTCAG AATTTGATTA
12651 ATAACCGACA GCCCCCCTAA TTTTTTCTT CACTTCCAAC TTAGGACGAA
12701 CCAGAGAAAG CTAAATATGC ACCACCTACT AATCAAATAG GGTGCCGCGT
12751 TTCTAATGAA CCTCCTACA GCTTCCCCAG GCCAGCAGCC CCCAATCAGG
12801 AAACGCCTGA AGCCTTCCCT TTTTCTCACT GTAAAGCTTT CCCACTCCTC
12851 TGCCTGGCTT TGAGTCTCTG TCAATACACA AGTGAGGGTG TCTGACTCCC
12901 TTGCTATAGC AAAGTCGGGC CAAGTAGATT TACTTTTCT CATTTGATTG
12951 GTCTTTTATT TCTAGAAGGA ACATACAAGA AAATTTAAAG GGAATCCAT
13001 TCCTAATCTT TCATATTATA GTAGTCCCCT TTTATCTGCA GGCATATTT
13051 TCCAAGACCC CCACTGAATA CCTGAAACTG TGGGTAATAT TGAACCCAT
13101 ATATACTCTC TCTATATATA CATATATATA TATATTTTCT AATTTTTTTT
13151 TACTTTATCT TTAATTAGCT TTAGCTCTTT TTTTTTTTTT TGAGATGGAG
13201 TCTCACTCTG TCACCCAGGC TGAGTGCAGG GGTGCAGTCT TGGTCACTG
13251 CAACCTCTGT CTACCGGGTT CAAGCAATTT CTGTGCCTC AACCTCCGGA
13301 GTAGCTGGGA CTACAGGCGT GTGCCACCAC TTCCTGGCTA ATTGTTTTAA
13351 ATTTTAGTAG AAACGGGATT TCACCAAGTT GGCCAGACTG GTCTCGTACT
13401 TCTGACCTCA AGTGATCCGC CCACCTTGGC CTCCCAAAC GCTGGGATTA
13451 CAGGCGTGAG CCACCATGCG CCCAGCCATA GACTATATAT TTTTGATCTG
13501 ATAAGTGGTT CAGCTACTAA GTGACTAACA GGCAAGTAGC ATCTATAGTG
13551 TGGATATGCT GGACAAAAGG ACATTCACCT CCTGGGCAGG ATGGCACAGA
13601 ATGTTGAGAG ATTTTATCAT GCTACTCAGA ATGGTGTGCA ATTTAAAACT
13651 TATGAGTTGT TTGTTTCTGG AGTTTTCCAT TTAATAGTTC AGACCATGGA
13701 TTGACCGCAG GTAAGTAAA CTGTGGAGAG TGAACTGTG GATAAGGGAG
13751 GACTATTGTA TTGTTAAGTC AGACTCATTG GGCAATCATA ACTCTTGATT
13801 TGCCATCAGA AATGCTGCAG AAATATGGGT TAAAAAAAAC TGTTCAAAAA
13851 TAGGGTCAGG GATGTCCTTT AACTTGTTAC TTCCAAAATG TTAGTGAAAA
13901 CTGTGGCCCC AAAGAGTGAA AGGAACAAAT GACTAAGAGA AAATCTTGTT
13951 TTCAGGATGA CAGATTAAAA AAGAAGCAAC TTGCTGAAAC ACTGAAAATC
14001 TCTCCACTTG TAAGATAACA CAAAACCTGG TAAACTGGT TGGAAATGAAT
14051 ATGGCCAACT CAAGTCTGCA CAGAACTAAC TTGGTGATGT TACAGCCCAA
14101 ATTTCCACCA CATATTTTAT ACTAACTCCC CCGGATTTT CACACATGAT
14151 CTGTGAAGTA GCATGAAGTA GTAACATATG ATGCCTAAGG ACTTGGGAGA
14201 CCTCCCCATT TCCTTCCACC AATCACCAC TAATCCAGA ATCCGCCCCC
14251 AAACCTTTTC TAATAACTAC CTTAAAGCCA GCATAGGGAG ACAGATTTGA
14301 GCTGGACTCC TGTCTTCTTG TGGGTCACCT TGCAATAAAA AGCTTTTCTT
14351 TTCTCAACAC CTGGTATTAT AGTATTGACT TCTAGTTCAT CGGGCAGCAA
14401 GCCCCTTTTG GTCGGTGACT ATTCTTGTTG GCTGATATTT CCATTGGCCA
14451 AAATATAAAC CTCTTAGATG AAACCTCAGT ACGTAAATGG CGCCACAGAA

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FIGURE 3E

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14501 TGCTGTGACA TTTTCTCTT GGATTATAGC AGGTACTTT ACTGAATACC
14551 GTAGGCAGTT ATAACACACT AAGTATTTGT GTATCTAAAC ATAGAAAAGA
14601 TACAGTAAAA ATATGGTAAT TTTTTC AAC TTTTAGTTGA GATTGGAGG
14651 GTATGTGCAC ATTTGTTACA AGGGTATATT GCATGATGCT GAGGTTTGGG
14701 GTACAATTGA ACCCTGTCAC CCAGGTAGTG AGCATAGTAC CCAATCGATA
14751 ATTTTCAAC CTTTGTCCAT TCCCTCCCG TTCTGTAGT CCCCAGTTTC
14801 TGCTTTTCCC ATCTTTATAT CCGTGTGCAC CCCATGTTTT GCTCCCATGT
14851 GTATGTGAGA ACTTGTGGTG TTTGGTTTTT TATTTCTGCG TTGATTGCT
14901 TAGGATAATG GCCTTCAGCT GCATCCATGT TGCTGCAGAG GACGTGATTT
14951 TATTTCTCTT TATGGCTGTG TAGTATTCCA TGGTGAAAAA TATAGTACTA
15001 TAACCTTACT AAATCACTGT CATATATATG GTCTATCATT GACTGAAATG
15051 TATACAGTGC ATGATATATA TATATATATA TCTATAATGT CTTATCCATT
15101 TCGTGTATTA TGAGATTTGA TTGCTAATAT TTTATACAGG AGTTTTGCAT
15151 CTTTTCACT AGTTGACATT GCTTGTAAAT TTCTTTTTT TGTGATGTCC
15201 CTGTTAGGTT TTAGAATCAA GTGTATACCC GCCTCATAAA ATGGGTGGA
15251 AAATGTTCCC ACCCTTCTG TTCTCTGGA AATTGGTGT TTTTCTTAA
15301 AGTTTGGTAG ACATTATTGT TAAAACCATG GGGCTCTCGA TTTTCTTCA
15351 TGGAAATGTT TTCAAATTAC ACTTTAAAT TCTTTAAAT CTGAGTATAG
15401 GGCTATCAGA CTTTCTGCTG TCTTATGTCA GTTTTAAATA AGTTGTTTTT
15451 GTAGGCGTTT GTTATCTCAC TTTCATATTT TTGATATAAA GCTTTTCATA
15501 ATATCATTA TGTCTATAGT GTCTAGTAGT TTCCATCTTT ACTTTCTGAC
15551 ATTGGTTATT TGCCAGTTTT AGGAGTTTAT CAATTTTATT AGTCTTTTCA
15601 AAGAACCATC TTTTGGCTTT GTTAATCCTC CCAATGGTGT GTTTCTTTC
15651 TCATTACTTT TTGCTCTTTA TTTCTTCAA CTCTTTTTT GCTTAATTTT
15701 AAAATAATTT CTTGAGATTG AGATAAGCCT CAATGATGGG TCACCGATT
15751 CCAGTCTTTC TTCTTTTCTA ATTATGCATT TTAAACCAGA AATCTTCTC
15801 TAAGTGTAGC TTTAGTTGCA GCTCACAAGT TTCAGATCTG TCTCTCAGTC
15851 TGGAGTTGG AGATCTGACC ATGACCATGA AACCATCCAG TCACAATGTG
15901 GCATTATTTT TTTAATTTTT TTTTTTTTT TTGAGATAGA GTTTCACTCT
15951 TATTGCCTAG GCTGGTGTG AATGGTGCGA TCTCGGCTCA CAGCAACCTC
16001 CACCTCCAG GTTCAAGCGA TTCTTTTGCC TCAGCCTCCC AAGTAGCTGG
16051 GATTACAGGC ATGCGCCACC ATGCCCACT AATTTTGTAT TTTTAGTAGA
16101 GATGGGGGTT CTCCATGTTG GTCAGGTTGG TCTTGAATC CCGACCTCAG
16151 GTGATCCGCC CACCTCAGCC TCCCAAAGTG CTGGGATTAT AGGAATGAGC
16201 CACTGTGCCC GGCCCAACTT GGCATTATTT ACCCAGAAGA GCATGACCAT
16251 GAGAACAGTA GAATTTGTAA GCTTTGAGTG GGTGACTATG AGTGTCAATA
16301 TAGGTAGATA GGTATATTTT TGGGTGGTGG TAGGAGAGGG CTTACAGTTT
16351 GCTATGACAG CTTTTATAT GGATCATCCT TAGTAAAAGA TTATTTAATT
16401 TTTGAAATCA AAGGGGAAAA CACTAGTTTA GGCTTCTTCT TTTCTTCTT
16451 TTTTAGAGAG AGGGTCTTGC TCTGTCACCA GGTTAGAATG CAGTGGTGCA
16501 ATATTGCTCA CTGTAACCTC AAATTCCTGG GCTCAAGTGA TCCTCCTACC
16551 TCAGCCTCCA ATGAGCTAGT ATTTACAGGC ATGCACCAAC ACATCTGGCT
16601 AATTTTAAAA ATTTTTTATG GAGATGAGGT CTCACTATGT TGTCCAGTCT
16651 GGTCTTGAAT CCTGACCTCA AGTGATCCTC CCCCATCAGC CTCCCAAAGT
16701 GCTGCAATAT TTTAAATCCT GTGGTAGGTC AAGTGGTTGT CTTCTATCTT
16751 GGGGTTTATA AAGTACATGT CAAGAAATTT AGGGTATGGT TAGATTAGCT
16801 TTAATAATGT CATGTTTTAT AAAAATCAAT GCATCATTTT TCTGATTGAA
16851 AATTTAACAC AAGACTCAGA ATCTTTTTTG AGTAGTGGAA TTAATTTTAT
16901 TATAGATCTT TGCGATAATG AATGATGATA CATCTGGCCA AAAATAGGTA
16951 CTATAGTCTT TTAGGAAAAC AGCTAATCTG CTTGAAATAT GTGTAGAAAT
17001 AATTTAGTGC ATCAGCCCAT ATTGGCAATA ACTTCTCTCT AATTTTTTTT
17051 TATAGAAAAT TTTTACTACT GGAGATGTCA ACAAAGATGG GAAGCTGGAT
17101 TTTGAAGAAT TTATGAAGTA CCTTAAAGAC CATGAGAAGA AAATGAAATT
17151 GGCATTTAAG AGTTTAGACA AAAATAATGA TGGTGTGTCT TTCTTTTGT
17201 TTTATCACCA GCTATGAAGA AGCATTTATC ATGCTTTCAA GAGTCTAAAA
17251 GGATGCTTAT TTAATCTCTC TGGTTTTAGA TGATAATTAT TATTTGTGTT
17301 AATACTTTTT TTTAGTAATG TGATTTTTAT GTAGAGTTTA TATTATTTAG
17351 TGAAGAAAAC TTATAGATAG CTTTCTTTT TCATTACTTT GAAATGTAAT

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FIGURE 3F

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17401 GAATTACATT TCTGAATTAA AAACGTGTTG CAGGGCCTGT TGTAAATGTT
17451 AACTATGGAA CATTATGCTG ATTTGAGTTA AACCTGTAGG TTAATAATAA
17501 TAATTATATT TTCTTGTCTT CTGGGTAAAA TGAGATTTCT TTTTATTTGT
17551 ATAGAAGAAT GACAGTTGTG TCATCTAAAA TTTAAAAAAC TTTCAGATTA
17601 TCTTGCATCT GTTAGTTTTT TTGGAAGAAT TAATTTAGAG AAGATATCTC
17651 TGATCCTGGA AATTAGGGAA AAATAGCATA TAAACGTTTA AGTGTGTACC
17701 TTCTGGTTAA GATTATGACT TCTATATTTT GATTAATAGG TTGGAGTTTG
17751 TCTTAATCTG TTTTCTGTTG CTGTAATGGA GTACCACAGA CTGGGTAATT
17801 TATGAAGAAA TGAAATTTAT TTCTTATAGT TCTGGAGGCT GGGAGGTTCA
17851 AAGTTGAGCC GAATCTGGTG AGGGCCTCTT ACTATGTCAT AACATGCTAG
17901 CAGGCATCAC AGAGCAAATG CACTACCTCA GATCTCTCTT CCTCTTCTTA
17951 AAAAGCCACT AGTCCCATCA TGGGGGCCCT ACTCTGAAGA CCTTATCTAA
18001 TTCTAATTGG AAATAGGGTC TTGAAGCCCT CATCACTAGA GGTAACCTTT
18051 AACAGGAAGA GAGAATTTAT AAAAATTATA ATGCAGCACC AAATCCCTCC
18101 CTACTTGTGA ATAGTCAAGG TCATTTTATT TACAGACTTG TTATTAAAGA
18151 AACAGGTTAA ACAAATAGAT TGAGAGGAAA TGTGGTTCAT GTCTGAGATC
18201 AGCAAACCTT TTTGTCCAGA AGTCCAGATA ATAAATATTT TAGCTTTGTG
18251 GGTCACTGTG TCTCAGTTGT AGCTACTTGT CTCTGCTGCT GTACCTCAAA
18301 AGCAGCCATG AAATGATATG AAATGAATGG GGATGACTGA TTTCCAATAA
18351 AAACCTTTAT TACAAAGATA GTTAATACAC CTATTTTGGC TTGAGGGTTA
18401 TAGTTTGCCA TCCCCTGATT TACAATGAAT ATTAAGTTT AATTCAAAGC
18451 AAGTTCCCTC AAACAAACAA ACTAAACTCT AGATGATTTT GAAGATTATT
18501 CACATCTGTG ACTCTCAGCC AGGAAGAGCT GAGTTTGGGT TGGAAAGTAG
18551 TACTATTGGA ACATTTGTTG CCCATAAGCC TTACAATATA TGCCCTTAAG
18601 TCTAGCCTTA GTCCAGTCTT CTAGCAAAAC TCAGTTTTCT TTCTTCTCTG
18651 CAAACTTTCA TTCCAACATC GACCCTCTGC AGTTCAGATT GTCTTGACGG
18701 TCAGATTGTC TGTGTGCTGC TATGGTAGGC AGTAGCTGAG AGATGGAGCT
18751 ACCTTAAGAT CAATTGCCAG ATAATCAGAG GTCAATTATC CCAGTGCATA
18801 AGTAGTGTAC ATATCAATTG TTCATTTTAT AAAATTCTAA ATGAACCAGA
18851 GGCAATAATT AAAGATGAAA TTTTGATGGT ATATTGTAG GAAATCTACA
18901 CAATGTTTCC CTAATTTCCC ATGTTTGTGT ATTTTAAAC AATGTGGCAT
18951 TATTGGTTCA TATTTTATT TTTTAGACTT CCTTAATGCA AAACATATAC
19001 AGTTGATCCT CATTATTTGG GGATTCTGTA TTTGCAAATT TGCCTACTCA
19051 ATAAATTTA TCCCCAAAGT AACCCCAAAA TATATACTCA CAGTACTTTC
19101 CCAGGCATTC ATGGACATGC ACAGAGCAGT GAAAAACTTG AGTTGCTCAG
19151 CATGTACATT CCTAGCTAGT AGAATAAGGC AATACTCTGC CTCTTGTTT
19201 CAGCTCTCAT ACTATTAACT AGCAAGTATC CCTTCAAGG TCTATTTTGT
19251 GCCAGTTTTT GCATTTTGTG ATTTTGTGTG GTAATTTCTT TTTTAAATG
19301 TTCCCCAAAG GTAGTGCTGA AGTGCTGTCT AGTGTTCTTA AGTGCAAGAA
19351 AGCCATAGCA TGCCTTATGG AGAAAAATA TGCGTTGGAT AAGCTTTGCC
19401 CCAAATTCAT TGTTAGTGAA TCAACAGCAC ACATTAAATG AGGTGCCTTC
19451 AAACAGAAAC AGACATAAGA CATGGTTATG TATTAATCAG TTGATGAAAG
19501 TGTTGTAATC AGAGGCTCAC AGGAACCTAA CCCTGTTTTT CCTGTAGGAA
19551 CAATGGTTTG GTATTTGCTA ATTCAGTGTG TGCAATGAAT ATAGAATTTT
19601 ATGGAAGATG ATTGCTGTGA ATAATGAGAA TTAACCATAT CTCTTAAGA
19651 GTGCATTTCT AAAGGAGAAT ATTCAGAAGG GTATTTGCAT AATTTCTTTA
19701 CTAACAGATG CTGCCTCTCA CTGTCCTTAC ATGGTCCAGA TTCTCATGCT
19751 GCTCCTTCCC TCTCCCCAGG AGGATTCTCT CAGAATCCTG TCATCTCCTC
19801 CAGGGTCCCT TCTCCAAGAA AGTCTATCCT TTCACCACTA ACAGTAATTT
19851 TGGTCTTCCCT CTTTTTCTGG AGAAGTCAGC TGTTTATGCT GCTTCAGCAC
19901 CAGACCTCTT CTACTTTGT TTTGTTTCAT TCTTTTTCAT GTACAGTAGT
19951 CTTAGGATTC TCATGAGCCT GTGAGCTGCT AGAAGGAAAT ACAGCAGTGC
20001 TTACATTTAT TGCTTCTATT TTATTTTCTA TTTTCTCTTC CTGTCTTCTG
20051 ATGTTTCTCC TTCTGTCCAC AAACATGCTC TAATTTCCCT AGTATTAAAA
20101 ATTTTCTGTC TTTTGTGTGT CTTTATCCT TGCTCCCTTA TTTTACTGTC
20151 CAGATTTTTA TTTTATTTA TTTATTTTGG AGATGGAGTC TCACTCTGTC
20201 ACCCAGGCTG GGGTGCAGTG GCGCGATCTC AGCTCACTGC AACCTCCGCC
20251 TCCCAGCTTC AAGCAATTTT CCTCTTTTAG CCTCCAAGT AGCTGGGATT

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FIGURE 3G

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20301 ATGGGCACCT GCCACCATGC CTGGCTGATT TTTCTATTTT TAGTAGAGAC
20351 GGGGTTTCAC CATGTTGGCC AACTGCTCT CTAAGTCTG ACCTCAGGTG
20401 AACCACCCGC CTCAGCCTCC AAAAGTGCTG GGATTGCAGG TGTGAGTCAC
20451 TGTGCCTGGC CTTTTACTGC CAGATTTTTA AAAGAATAGT CTGTGCTTTA
20501 GCTCTATTTT CTCACTTACT ACTTCTCTTT AACTCAGTCA TATATGATGT
20551 TTTGCATAGT AAATGTCTAG TAATTTATTA AAAATGTAGA AATAGGTACT
20601 TTTAAAATGA ATAGATCCTA CTTTAATTGA ATTTATCTTG GAGTTAGAAT
20651 ATCTTGATTT GGATTTTAGT TCTGCTACTT CTTAATTACA TTAATTGGTA
20701 AGGCCACTTG TGAAGTCAGT CTCTTTGGAG GAATATTATT TATCTATAAG
20751 GCTGTTACAA TTAAGTGAAT TTAAGAAATG TGTATTTATT TTTTAATGTA
20801 TTTGTTACAT TTTTAGTATT GATGTTGGGA TAGGCATTTA AGCAAGTCTA
20851 TAACTCACCT ACATGCATAA TTTTGCCTTA ATCAGTTTAA AGCTTTCTCT
20901 TAAATGAGAG ATTTGAAATT CATAATTTCT GTGTTCTTA TCAGTTCTGA
20951 GTTTTATTTT TTGCCCTTTT TATTTTTTTA AAGGAAAAAT TGAGGCTTCA
21001 GAAATTGTCC AGTCTCTCCA GACACTGGGT CTGACTATTT CTGAACAACA
21051 AGCAGAGTTG ATTCTTCAAA GGTAAGCTCT TCATGTTGGT CAACAATTGA
21101 CTTTCACTTT AATATCCTGC ATTAGAACTC TGTGTTTGTA AGTGTGGCTT
21151 TAAAAACACT CCCTAGTCTT CATTATGTAT ATCCAAGATC TTTTGTCTT
21201 TTTTCTCTCC ATCTATTTTG TATGTGTACA TTTATCTAAA GTGTAAGAAT
21251 GGGAAAGTGA AGCTCAGACT GGACTCTTTC TTTCAAGGCC TCAAAGGATA
21301 GTGGAATGGC AGGAAGTAAG GTTTAACTC CATAGATGAG GAGCTGAAGA
21351 GTTTTGGTGT TGCTTTTTCT CCATTTGATT TCTAATGTGA CAGTAAACT
21401 CATTGATTCA AACTAAGAAG ACTAGCAGAT TCATCACATT ATTTAACCTA
21451 GATGTGACTG GAAAAAAGGG AAATTAATAA GCTCTCCAAG CTAACAAAGA
21501 AATACCTGTT TAAACTTTCA GAAAAAGAA ATGCAAATTT GAACCTTATT
21551 GTCTGGGGCA ATCAGTTTGA CTATTTAAGT CAGACTTTTA TACTCTTAAT
21601 GTTTTGTTC ATGGGATAGA GCAGTAATCT CTGCAGCCCA GGTGCTCTCA
21651 AATACTCTGT TGCTATAAAC ACAGGGCAGG AACTGATTTT TTATGATAAC
21701 GTAAACACAGA AAAGGACAAT TATATTGTAT TAATATTGTT GTGAATATT
21751 TCAGTCTCA CAATGCTTAA AAATCTTTCT AAATGGCTTT GTTATTGAAT
21801 TTATCTCATT TTATATCTGT GCCAACAGCA TTTTCATCCT TTCTCTTCAT
21851 AATTTCTTTT ACAAACAGCT GCTCAAGAGG AAGGCTCAAA GTCTCAAGGC
21901 TGAGCACGTA ATGACTTTTG TTAGTACTAG ATGAGAAGGG CTTTCTGAG
21951 GAAATGAAAA CCTAAAACAT GAAAAAGAA TAAACAGAAT TTGGACAGTG
22001 AGATATAGAG CATATAATAT TCTGCTTCTA AAGTAATATT CTTCTAGGAA
22051 AGTGAGGGCG TTTCCCTGGC TGTTAGGCCA GAAATCATAT TCCTATATTT
22101 TCTTTGATAG CTTTAGGAAT AATGCAAATT CTAAGCCCAA GCTTCAGAAT
22151 AGACTAAGAA GTATTAGCTT AGCTGCCATG ACAAATACC ATAGGCTGGA
22201 TGCATTAAAC AATGGAAATT TAGTTTTTCA CAGGTCTGGG AGCTGGGAAG
22251 TTTAAGATGA GAGTGCCAGC ATGGTTGGGT TGTAGTGAGG GCTCTCTTC
22301 TGGCTTGACG ATAGACCCCT TCTACTGTA TTGTCATAT GCAGAGAGAG
22351 AGAGAGAGAG AGAGAGAGAG GATCTTTCTC TTGCTTTCTA
22401 TTATAAGGCC ATAGTCCTGT TGGATCAGGG TTCCATTCTT ATGACTTTAT
22451 TTGACTTTAC CCCCCTAAGA TGCTATCTCC AGATATAATC ACACGGTGGG
22501 TTAGGGCTC AACATTTGGA TTTGGGAGGG ACACAGCTCA GTCCATAGCA
22551 AAGGATAATG CAGAGGGTTG GATATTTAAA AGTAGCTACA CAATTTTAA
22601 TATAAATATT TTATGGTAAC TTTTTTTTTT TTTTGAGATG GAGTCTAGCT
22651 CTGTTGCCCA GGCTGGAGCG CAATGGTGCG ATCTCAGCTC ACTGCAACCT
22701 CCGCCTCCA GGTTCAGCA ATTCTCCTGC CTCAGCCTCC TGAGTAGTTG
22751 GGACTATAGG CACGCGCCAC CACGCTGGC TATTTTTTTT TTATTTTAC
22801 TAGAGACGGG TTTGCACCAT ATTGGTCAGG CTGTCTCGA ACTCCTGACA
22851 TCAGGTGATC CACCATCTT GGCTCCCAA AGTGCTGGGA TTACAGAAGT
22901 GAGCCACCG GCCTAGCCAG CAGCTTTACT GAGATGTAAT TCACATGCCA
22951 TAAATTCACT TTTCTAAAGT ATACAATTCA GTGACTTAAA ACATTTATTT
23001 ATTTTTAAAT TGACAGAATT ACATGTATTT ATCATGTACA ACATGATGTT
23051 TTGAAGTATA TGTACATTGT GGAGTGACTA AGTCTAGCTA ATTAACATGA
23101 TACATCTCAT ACTTAATGAT TTCTGTGGTG AGAACACTTT ACATCCATTC
23151 TCTTAGTATT TTTCAAGAAT ATAATATATT ATTATTAATT GTAGTCTTCA

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FIGURE 3H

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23201 TGTGTATAG TGGAGCTCTT GAACTTATTC CTCATGTCAA GCTGAAATTG
23251 TGTGTCCTTT AACACAAACC ATACCCGACT CCCAAAGTAT TCTGCTCTCT
23301 GCTTCTATGA GATTAACCTT TTCTGATTCC ACATGAGTGA GATCATGCAG
23351 TATTTATTTG TCTTTACCTG GCTTATTTCA TTCATATTGT TACAGATAAC
23401 AGGATTTCCCT TCTTTTTTTA ATGGCCGAAT AGTTTTCTAT TGTATATGTA
23451 TAGCACATTT TCTCTCTTCA TGCATTGGTG GACACTTAGG TTGATTCCGT
23501 ATCTTGGCTA TCGTGAATAG TGCTATAATG AACATGGGAA TGCACATGGC
23551 TCTTTGACAT ATTGATTTCA TTTTATATAT GTGTATATAT ATATGTATAC
23601 ACACACATAC ATACAGTGGT GGGATTGCAG GATCATATGG TAGTCTATA
23651 TTTAATTTTT AAAGGAACTC CATACTGCTT TCCATAATGG CTGTATTAGT
23701 TTAACCTCTC ACCAACAGGG TGCAAAAGTT CCCTTTTCTC TACATACTTG
23751 CCAACACTTG TTATCTTTTG TCTCTTTGGT AATAGTCATT CTAAGTGTAG
23801 TATGAGGTGA TATCTCATTG TGGCTTTTAT TTGCATTTCT GTGGTAATTA
23851 GTGATATCGA GCTTTTTTTT TTTTTGTAC TTTGGCCATT TGTATGTCTT
23901 TGAAAAATGT CTATTGGGGT TTTTGGTTG TTTATTGAG GTTTNNNNN
23951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
24251 NNNNNNNCCG GGGTCCCGT CATTCTCCCT GCCTCAGCCT CCCCAGAGTA
24301 GCTGGGACTA CCAGGGCACC CGCCACCAC GGCCCGGGCT AATTTTTTGT
24351 ATGTTGAGTA GAGACGGGGT TTCACTGTGT TAGCCAGGAT GGTCTTGATC
24401 TCCTGGCCTC GTGATCTGCC CGCCTCGGCC TCCAGAGTG CTAGGATTAC
24451 AGGCGTGAGC CACCGCGCCT GGCCTGATTT CTAGTTTTTT ATTATTGTGG
24501 TCGGAAAAGA AACTTGATAT GATTTCATTC TGCTTAAATT TGTTAAGACT
24551 TGTTTTGTGG CCTAACATAT GATATCCCCT GGTGCATGTT CCATGTGCAG
24601 TTGAGAAGAA TGTGTATTCT CTTGCCATTA GGTGAAATGT TTTATGTCTG
24651 ATCTGTCCAT TTGTTCTAGA GTATAGTTTA AGTCTGATGT TTCTTACTGA
24701 TTTTCTGTTG AGATGATTGG TCTATTGCTG AAGGTAGGGT GTTGAAGTCC
24751 CCTACTATTG CTGTATTGCA GTCTCTCTCT CCTTCAGAC GTATTAATGG
24801 TTTTTATTTT ATTTTATTTG TTGTTGTTGT TGTGTTGTT GTTGTTTTGT
24851 AGACGGAGTC TCACTCTGTC ACCAGGCTGG AGTGCAGTGG CAGGGTCTCG
24901 GCTCACTGCA GCCCCCGTCT CACGGTTCAA GCGATTCTCC TGCCTCAGCC
24951 TCCCAGATCG CTGGGACTAC AGGCGCATGC CACCACGCCC AGCTAATTTT
25001 TGTATTTTTA GTAAAGACGG GGTTTCACCA TGTTGGCCAG GATGGTCTTG
25051 ATCTCTTGAC TTCATGATCC ACCCGCCTTG GCCTCCCAA GTGCTGGGAT
25101 TACAGGTGTG AGCCACCACC CCTGGCCAAT GTTGGTATT TATCTTAGG
25151 TGCTCTGATG TTGGGTTTAT ATATATTTAT AAAAAACAAT AGCTACATAA
25201 CTTATTAAGG GATATGCAAT ATAAATATA TAAATTGTGA CACTGAAAT
25251 TTAAATGGG AGGAGTGGAG TAAAAGTACC TTCATATAAC TTACTATTAT
25301 ATCCTCTTAT TGAATTGACC CTTTTATCAT TATATAGGAA CTTTGTCTCT
25351 CCTTTACAAC TTCTGACTTA AAGTTTGTGT TATATGATAT AAGTAAAGTT
25401 ACTCCTGCTC TCCTTTGGTT TCTGTTTCCA TGGAATATCT TTTTCCATTC
25451 CTTCAACATC AGTCTGTGTG TATTTTTACA GATGAAATGA GTCTGTCATG
25501 GGCAGCATAT AGTTGGATCT AGTTTTTTTA ATCCAATCAG AACTGTGTT
25551 TTTTGATTGG ATAATTTAAT CCATTTCATG TCAAGGTAAT TATTGATAAG
25601 TAAGGACTTT GTACTACCAT TTTGCTTATT GTTTCATGGT TCTTTTATAG
25651 ATCCTTTATT CTTTTCTTCC TCTCTTGCTG TCTTTTTTTT GTGGTTAAGT
25701 GATTTTCTCT AGTGGTATGT TTTGATTTCT TGCTTTTTAT TTTTGTGTA
25751 TCTCCTATTG GTTTTTGGTT TGTGGTTACC AAGAGGTTAC AAAAAACATC
25801 TTAAGAGTTA TAATAGTTTA TTTTAACTTG ATAACCTAAT TTTTATTGCA
25851 AAAACCCCCC AAAACAAAAA AATCTACACT TTTACTTAAT CCCCTGAAAT
25901 TTTGAATTTT TGATGTCACA GTTTACCTCT TTTTATATTG TGTATCCCTT
25951 AAATTATTGT AGCTATTATT ACTTTTAATA GTTTTCTCTT TCCTACTACA
26001 GATGTAAGTG ATTTGCATAC CATCATTACA GTATTATTTT GAATTTACCT
26051 GTGTACTTTT TTTTATCAGC CAGTTTATA CTTTCAGATG TTTTGTGTT

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FIGURE 31

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26101 ACTCATTAGC ATCTTTTTCT TTCAGCTTGA GGAGCTCCTT TTACGTTTCT
26151 TATAAAATAG GTGCGGTCAT GATTATCTCC CTCAGCTATT GTTTGTCTGG
26201 GAAAGTATCT CTCCTTCATT TCTGAAGGAC ACTTTGCTGG GTACATTACC
26251 CTTGGTTGGT ATTTTCTCCT TTGAACGCTT TAAATATATC ATCCCTTCT
26301 CTCCTGACCT GTTAGGTCTC TGCTGACCAG TCTGTTTCCA ACCATATTGG
26351 GACTGTCTTA TATGTTATTT GCTTCTTATC TTTTGCTGTT TTCAGGATCC
26401 TCTCATTGTC TTTGATTTTT GATAGTTTGA TTGTAATATG TCTTGGGGTA
26451 GTCTTGTTTG GATTGAATCT GATTAGAGAC CTTGGACTTT TCCTGCATGT
26501 AGATATTTAC CTCTTCTCCT AGGTTTGGAA AATTTTCTGT TACTGTTTCT
26551 TTAATTAAGC TTTTACCCC TTTTATCTTC CTTTCTCCT TCTCAACTC
26601 CTGTGACTCA AAACCTTGCT CTTTGATGCT TGTTCCATAA ATCTTGTAAG
26651 CTTTCTTCAT TCATTTTCAT TCTTTTTTCT CCTCTGTGTA TTTTCAAATA
26701 ACCTGTCTTT GAGTTCATAG TTTCTTCTT CTCTTGATC ACTTCTGCAG
26751 TTGATGCTCC CATATTGCAT TTTAATTTTG TTCATTGTAT TTTTCAGCCC
26801 CATGATTTCT GTTTGATTTT TTCTTTTATT ATTTTCATCT TTTATTACCT
26851 TTCTCTTTGT GGTCACTCGT TATTTTCTTA ATTTTCATTGA ATTGTTTCTT
26901 TGTATTTTCT TGAAGTTTGC TGAGCTTCTT TTGAATTCTA TGTCAGTTCA
26951 TACATCTCTG TTTCTTTAGG GATGGTCGCT GGTACTTTAT TTTGTTTCTT
27001 TAGTGGTGTG ATTTGTTCTT GATTGTTGTT GATGTTTGTT GCCTTGTGTT
27051 TACATCTGTG CATTTGAAGA AGTAGGCACT TATTTCACTC TTTGCAGACT
27101 GGCTTTGTCT GAGAATGCCC TTCAACAGTC AGCCTGTCTA GAGATTCTTT
27151 AATATTTAAT TAAATATCTT TAATATTTTG AAGAACTTCC AAATTGTTTC
27201 TAAAGTGGCT GCACCATTTT ATAATCCCAG CAGCAATGAA TGAAGGTTTC
27251 AGTTTCTCCA TAGCTATATG AATACTCATT ACTGTCTGTC TTTTCATTTT
27301 TTGATTTTTA TTTTTTTTTT GAGAAAGGGT CTTGCTCTGT CATCCCATCT
27351 GGAGTGCAAT GGCACAATCA TGGCTCATTG CAGCCTCAAC TTCCCTGGCT
27401 CAATTGATCC TCTCACCTCC TGAGTACCTG GGACTACAGG CATTGTACCA
27451 CAATGCCTGG CTAATTTTTA TATTTTTTGT AGAGATGTGG TTTTGCCATG
27501 TTGCCTGGTG TATTAGTCCA TTCTCATGCT GCTATAAAGA ACTGCCTGAG
27551 ACTGGGTAAT TTATAAAGGA AAGAGTTTAA ATTGACTCAC TTTTGCTTGG
27601 CTGAGGAACC CTCAGGAAAC TTACAATCAT GGTGGAAGGG GAAGCAAACA
27651 CGTCCTTCTT CCATGATGAG CAGGAAGAGC AGTGCCTAGC AAAGAGGGAA
27701 AAAAACCTTT ATAAAAAAT CAGATCTCAT GAGAAGTTAC TCACTATCAT
27751 GAGAACATCA GAATGAGGGT AGCCTCCTCC ATGATTCAAT TACCTCCAC
27801 TGGGTCCCTC ACGTGACATG TGGGGATTAT TGGAATAATA ATTCAAATG
27851 AGATTGAGGT GAGGACACAG CCAAACCATA TCATTTTTGC CCTGGTCCCT
27901 CCCAAATCCC ATGTTCTCAC ATTGCAAAAC ACAATAATGC CTTTCCAGCA
27951 GTCCCCCAGC GTCTTAACTC ATTCCAGCGT TAACCTAAAA GTCCAAGGTT
28001 TCATCAGAGA CAAGGCAAGT CCCTTCTGCC TATAAGCCTG TAAAATCAAA
28051 AGCAAGGTAG TTATTATACT TCCTAGATAC AATGAGGGTA CAGGCATTGA
28101 TTAATATATC TTGTTCCAAA TGGGAGAAAT TGGCCAAAAT GAAGGGGCTA
28151 CAGGCCCCAA GTAAGTCCGA AATCTAGTGG AATAGTCAAA TCTTAAAGCT
28201 CCAAAATGAT CTCCTTTGAC TCCACATCAC ACATCCAGCT CATGCTAATG
28251 CAAGAAGTGG GCTCCCATGG CCTTGGGCAT CTGCACTCCT GTGGCTTTTC
28301 AGGGTACAGA CCCCCTTCTG GCTCTTTTCA CAGGCTGGCG TTGAGTGTCT
28351 GTGGCTTTTC CAGGTGCATG GTGCAAGCTG TCGGTGGATC TACTATTCTG
28401 GGTACTGGAG GATGGTGGCC CTCTTTTAC AGCTCCACTA GGCAGTGCTC
28451 CAGTGGGGAC TCTGTGTGAA GGCTCCAACC CCACATTTCC CTTCTGCACT
28501 GCCCTAGCGG AGGTTCTCCT CAAGGGCTCC ACCCTGCGAG CAAACTTCTG
28551 TCTGGACATC CAGGCATTTT CATACTCCT CTGAAATCTA GGCAGAGGAT
28601 CTCAAACCTT AATTCTTATC TTCTGTGTAC CCGCAGACTC AACACCTTGT
28651 GGAAGCTGCC AGGGCTTGGG GCTTGACACT TCTGAAGCCA TGGCTGAGC
28701 TGTACCTTGG CTCCTTTTAG CCATGGCTGG GATGCAGGGC ACCAAGTCTT
28751 GAGACTGCAC AAAGCAGCAA GGCCCTGGGC CTGGCCAGG AAACCATTTT
28801 TTCCTCCTGG GCCTCTGGGC CTATGATGGG AGGGCCCTTC CTGAAGACCT
28851 CTGAAGTGCC CTGGAGGCAT TTTCCCATTT GTCTTAGTGA TTAACATTTT
28901 ACTCCTTGTT TCTTATGCAG ATTTCTGCAG CTGGCTTGAA TTTTTTCTC
28951 AGAAAATAGA TTTTCTTTT CTGTCACATC ATCAGGGTGC AAATTGACA
  
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FIGURE 3J


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29001 AACTTTTGTG CTCTGCTTCC TGTGGAATGC TTTGCCACTT AGAAATTTCT
29051 TCTGCCTGAT ACCCCAAATC ATCTCTCTTA GGTTCAAAGT TCCACAGATC
29101 TCTAGGGCAG GGGCAAAAAG CCACCAGTCT CTTTGCTATA GCATAACAAG
29151 AGTCATCTTT GCTCCAGTTC CCAACAAGTT CCTCATCTCC ATCTGAGATC
29201 ATCTCAGCCT GGACTTCATT GCCCATATTA CTGTCAGCAT TTTGGTCAAA
29251 GCAATTCAAC AAGTCTCTGG GAACTTACAA ACTTTCCAC CTCTTTTGT
29301 CTTCTGAGCT CTCCAAATTT TTAAGAAGTT CCAAACCTTC CCAGTCTTCT
29351 TCTGAACCTT CCTAACTGTT CCAACCTCTG CCTGTTACCC AGTTCCAAAG
29401 TCAGTTCCAT ATTTTTGGGT ATCCTTATAG TAGCACCCAA CTCCTAGTAC
29451 CAATTTACTG TATTAGTTCA TTCTCACGCT GCTATAAAGA ACCACCTGAG
29501 AATGGGTATT TTATAAAGGA AAGAGGTTTA ATTGACTCAC AGTTTCGCGT
29551 GGCTGGGGAG GCCTCAGATA ACTTACAGCC ATAGCAGAAA GGGAAGCAAA
29601 CATGTCCTTC ACATGGTGGC AGGAAGAAGA AGTGCTGAGC AAAGAGGGAA
29651 AAGCCCTATA AAACCATCAT ATCTCGTGAG AACTCACTCA CTATCATGAG
29701 AACAGCAGCA TGGGGTTGAC CACCCCCCAT AATTCAATTA CCTCCCACCA
29751 GCTGTCTCCC GTGACACATG GAAATTATGG GAACTACAAC TCAAGATGAG
29801 ATTTGGGTGG GGACACAGCC AAACCATATC ATCTAGGCTG GTATCGAAAT
29851 CCTGGGTCAC AGCAATCCAC CCACCTTGCC CTACCAAAGT GCTGGGATTA
29901 CAGGCATGAG CCACCATATC TGAACGTGCT TTTGATTTCT TTTGATTTTA
29951 ACCATCCATT GTTTCTGCTT CTCTAGATAA CCCTGACTAA TATATAATTG
30001 GTATGAAGTG ATATCTCATG GCTTTGATTT ATATTTCTTT CATGGCTAGT
30051 GACTTTTTTT GTACTTTTGG GATATTGTTA TTATTATTAT TATTATTACT
30101 AGTGTTTATA CTTCTTCAGT AAAAGTGTTA GAAACAATTT TTAAGGCAG
30151 AATGTGACCA GAGTTTCCTG TAGTTATATA ACCATCATGG ACCTTCCCTC
30201 AAGTGCTAAG CCATTAGTGT TACTCATGTC ACTCCAAATG TCAGCTTGTT
30251 TTCTTCCATT TCACTGTCTC TTTGTGTCCC AAACCTGAAT TCATGGGAAA
30301 AACATCTGAA TGGTGCTTAA TATGGTTTGG ATATTTGTCC CCTCCAAATC
30351 TCATGTTGAA ATATGACCTC CAGTGTTGGA AGTAGGGACT ACTTGGGTCA
30401 CGAGAGTGGA TCCTTCATTA ATGGCTTGGT AATAAGTGAA CTCTATTAGT
30451 TCATGAAAGC TTGTTGTTGA TAAGAGCCTG GCATCTCATT TCTCTTGTCC
30501 TTCTCTCACC ATCTGACACA CTTGCTCACC TTTTTTCTTC AGCCATGAGT
30551 AAAAGCTTCC TGAGGTCTCA CCAGAACTG AGCAGATGTT GGTGCCATGC
30601 TTGTACAGTC TGTAGAAGTC TGAGCCAAAT AAGCCTCTTT TCTTTATAAA
30651 TTACCGAGTC TCAGGTGTTT GTTTAAAAACA ACACAAAACA GACTAACACA
30701 GTGTTGATTG AAACAGCTGT GACTGGGTCA TCAGGGTGTA AGAGAGGAGT
30751 CACTGAGTTG AAATATAGCC TCCTACTTAC ACCTGTTTCA TAGAAGCTGT
30801 AGATATGAAG TAGCTGAAGC AGGCATTCCC TCTGAAACAT GTGTTTCACA
30851 TATGTCATAA TTATCTTCTG CTCTCATTTT TCTTTTAGGC TTTTGTCTCC
30901 ATCTCATTTT CCCTGTTTAC TCTCATTTT ATATCTTTAC ATTTCTTTCT
30951 CCAGAATTGT TCAGAAGCTT GGAACCCTTC ACTCCAGTTA TTCTTTGACT
31001 ATGCAATTTG TTTCTGTGCT TCATGGCACT TATGGTTTGT AATCCTTGAC
31051 TTGTTTGAT ATCTCAGTGG TTAGGAGTAC AGTTTGGAGT TAGAATGCCT
31101 GGGTTGAAAC TCTTAATTCT ACTCTACTTA CTAGTCTTGT GACTATAACA
31151 AAATCTTAG CCTCTCTTTG TCTGTAAAAT GGAGAGTATA GTAAATACAT
31201 GGGCTTGTTT TAAGGATTAA ATGAGTTAAC ATGTGAAATA CTTAGAACAA
31251 TGCCTGGCAA ATGCTCAATG AATATTGAGT ATTGCTTGCT TTTGTTTAGT
31301 GCCATGCCTG TTGTTCCAC TGAGGGCACA GACCATGTGT ATCTGGTTAA
31351 CAGTTCTATG TCCACCACGT TGCAATAATG GACTCTCAGA AAATATTGAA
31401 GAATATGTTA AAGAATGAGT AGAATTATGC TACTGAAAAG GGTGAGTGGA
31451 AGGTAGGTAG GGGAAAGGAC ATATACAGCC CTGGAGGCAG CATATATGGG
31501 GAATGGGTCA CACAGTGTTC CTTGGTACTC TCTAGACCAT AGTGGGCCAC
31551 CTCTTAGCTA GTGGCCTATG GATTATTTCA GCAGTCTGTT GGAAACATCC
31601 ATGAATATGA TAATAATGAC CCATTTGTGG GTTCTAAGAA AAAGGACAAC
31651 TACAATACTA GACAATAATA GTATGTAAGT TAGGAGGGAA GGGGATGATT
31701 TGTATTAAAC TGTTCTAAAA TTCTTACCTT ATTTAGGATG ATGGGGTCAG
31751 ACATTAACCT TAGACTTTGT TATATATATG TGGTAAAATT TCAAGGTAAA
31801 CCATTGAAAC TGTAGTAGTT GAGTATATAA CTTCCAAATC AGGGGGGAAA
31851 GAAATGGAAT AAGAAAATAA ATACATAAAC ATAAGATTGA AACAATCCAA

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FIGURE 3K

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31901 TGAAGAGTAG AGAGAAGAGG GAAAAACATA GAAAGAATGA GATAATTAGA
31951 AAGCAATAGG TAAGATGTGA GAAATAAATT CAAGTACAGT AAAACTCCAC
32001 TAAAAATGTG CCTGCAGTAA TGTGCGGCA TGATTTCCCT TCATCCCAT
32051 TCTCAAATGG GGCAGCCTAA ATAGCGTTCT TATCCTGTTT CCCTGGGGGT
32101 TTGAGGTGGG TGACGAGTAA GTTAGAAGAT AATCACCTTC TGATCAGTTA
32151 GGACTTTCTC AGTTTAGTCT TCAATTAATA AAAATTAATG TAAATTTTAT
32201 CAGAAGGCAG AGATTGTCAG ATGAAAGAAC AAGCAAAATA AAAGTCTTAC
32251 TGAAAAAAG CTGGGGTAGC TATGTTAATA TCAACTGTTA ATTATTATTA
32301 ATAATCTATT AATAATAGAT TATATAGTAA AAACATTAAT AAAAATAGAG
32351 TGTCACTACA TTTTAAATTT CAGTATGAGG ATATACAATT TTTAAGCTGG
32401 TTGATAAAAT TCTGGGGATT AATTGGCAA TCCATCATAG TGGTGAGAGA
32451 TTTTAACACA ATTCTTCTCG TATTTGATAG GTCAAGCAGA GAAAACTTT
32501 AGTGAAGACA AAAACTTCTA AATACATAAG CTTGATTTAA TGGGCATGTA
32551 ATAGGACCTA GCATCAAAAA ATTAGAAAAA ATATTTTTTC TTAGGTATTT
32601 ATGGAACATG TATAAAATTT GATTTTCGTAG TAGGCCATAA AGCCAGGTTT
32651 AACACATTTT AAAGAACTGG TATCACAAGA ACTGCTTTCT CTGACCACTA
32701 TGCATTAAAA TAGAAGTTAA TTACAGACAT AAATTATAAA AATGCCAATA
32751 TTTTAAAGTG TGATATACAC TTCTCAACTT ATGGGTCAAA GGAAATCGTA
32801 AGTGGAAATT CAAGGACACG TTGACTTGAA AACATTAAAA CTTATGGAAT
32851 ATTTCTAAGA TGGAACCTGT ATGAATTTTA TAGTCTGAAA GCTTTTATTA
32901 GAAAAGAATT AAGTCTGAAA ATTAATGTGC TAAGTTAGGG GAGAGAAAAT
32951 GGAATAATCT CGAAGAAGGT AGGAGGAAGG AGATAATAAA GAATATATAG
33001 CAAAGATGCA GTAACAGGAT CAACAAAGCC AGAACTGTTT GGAAAAGACA
33051 AGCCTCTGGA AAGATTGATG AAGAAAAAAG AGAAATGAGA TGTAATAATA
33101 TCATGTTTCA TTATAAATAG GCACATAAGG ACTTTTAAAA AACTAATAAA
33151 ATAATATGAA TCATTAATGC CAATAAATTT GAAAACAGAC AAAGTAGGTG
33201 AATTTCTAGA AAAATATAAC TTAGTGGGAC TGAATGAAGA AGCAACAGCT
33251 TATAGTACCT AAGCAATTGA AGAGATTGGG TCAGTAATTT AAAATTTTCT
33301 CATAAACAAA ACCTTAGCCC CAGATGGTTC TTGCAAATGA TTAAGAACA
33351 GATGTACAAA CATTTCCAGA GTGTAGAAGT ACCTGTCTCT ATCCTTTCTA
33401 GGAGATCATT ATAACACCAA AAGCAGACAG TATATGAAAC AGGGAAATTA
33451 GAGGCCAAGA TACCTATGAC TTATATGTAA AAATTTAAAG AAAATATTAG
33501 CAACTGAAT CAGCCATTTT AAAAAATATA CCACAATCAA TGCATTCATA
33551 AGAGCAGCTT AACAAAATTT GTTAGAAGGC ATTAAGAAG ACTCAGTATA
33601 GAAAAGATGT ACCTTCTCTC CAAATTGGTG ATAGAGATTC AATGCCATTA
33651 AAAAAACCCA CCTGGTTTTT TTGAGGAACT TGTCAAGCTG AGTCTCAAAT
33701 TTATATCAAA GAGCAAAGGC CTAAGAATAT CCAGGACATT CCTGAAGAAC
33751 TGTAAGGAGC CAGGGGCCCTG CCCTATCAGA TACCAAGGGT TGTTATTAAG
33801 CCATAACCAA GTCAGTGCTG TTTCTACAGA AACAGACAAG TTAACAAGTG
33851 AAACATAATA GAGAGCCCAG AAACAGACCC ATCCATATTT TGGATTTGTC
33901 ACGTGAAAGA AGTAGCTTTG CAAAACTTTG GGAAAAGGAG AGTGTGTGCA
33951 ATAGATGATG CTCGTGCTCA TGCAGACAAA AAGGAAATTT GGATACCTGC
34001 CTCTTACCGT ACACAAACAC CAACCTAAAC GTGAAAGTTA AACTATAACA
34051 GCTTGAGGTG GTGGGAAGA AATATCTTTA TCTCAGTGTA GGGAAGAATT
34101 TATTTTAAAA AGAAGACACA AAAGGCCATA CATAGGAATG AAAAGATTGA
34151 ATTCACTGTC ATTAATAAAGA TTAATTCAG CTGCGTTAAA ATCAAGAGCA
34201 TCTGTACTTG GACAGCATAG AGTGGAAAGA CAAAGAGAAG GTATTTGCCA
34251 GCTTATAACT TGAAGGATTA GAATGAATGA TATAAAGAAC TATGTAAATA
34301 AGAAAAAGAC ATACAACCGG TTAGAAAAAC GGGCAAAGAC ATGAACAGCA
34351 TATTTACAGT GAAGGAAACA GCGGTAGCAA ATGAACATGG TAAGAGATGC
34401 TCAACACGTT TAGTAATTTG AAGGGAAATG CAAGTTATAC CCACAGCAAG
34451 ACTATCTTAT CTAGGAAGTT TGTCAATACC CTAAATGTTT TGTGGTTTTA
34501 AGTCACTAGAG TTTGTAATTC ATTTATTTAT TCAATAAATA CTCAGTGCCA
34551 GGCACGTTTT TAGAAACCTT GGTTATAACT TTGAATGAAA TTAATAAAAA
34601 TCCTTGCCCT GTGGAGGATG CTTATGTGTG GGGAGTTGGG TGGTGGGGTC
34651 AAACAACAAT TACATTAATA TAGAAAAATG TGACATAAAT AAACCTATAA
34701 ATATTGCAAC CCAGAGTTAT ATTATAAATG TAAGTAGTGA CTAGGACTCT
34751 CATGCAGATA TACCTCTGTG CTGGGACAAA TGAAAGTTTA AGTGTAAATT

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FIGURE 3L

34801	CCCATATGCA	AGTCAAAATA	AAAAGTGACA	CTAGAAAACA	CAATAATGAA
34851	TATCTGAAAA	TTGCATTTTA	TTTGACTGCC	ATCCTTTTGC	ATCATTTTCA
34901	TACTAATTAT	AGAATAAAAT	TTGTAGGATG	CACCAAAGCT	TTTTTTAGAG
34951	ACATCCATTA	ATTCAATAAA	TAAATGAGCA	CCTTCTTTGT	GCCAGCAGCT
35001	GTAAGAGGTG	GCCCAAGGAA	GGGAATAAAA	CAGTCAAAAT	CCTGGTACAC
35051	TCAGAGTTTC	TCTTAGGAGA	AAACAGATAC	AAATGGCATT	AATTACCAAG
35101	AAACTTGTAA	AACAAGCCAA	ATATTAATGA	TAAATATTTG	AGTACAGTAT
35151	GTTAATTTTA	AGATTGAAAA	TGAGGTGCCA	GGATTTCTTA	AGACTCAAAG
35201	GCGAAGATGG	CTGAATAGGA	ACAGCTCTGG	TCTACAGCTC	CCAGCGTGAG
35251	CGACGCAGAA	GACGCATGAT	TGCTGCATTT	CCATCTGAGG	TACCGGGTTC
35301	ATCTCACTAG	GGAGTGCCAG	ACAGTGGGCG	CAGGTCAGTG	GGTGTGTGCA
35351	CCGTGCGCGA	GCTGAAGCAG	GGCGAGGCAT	TGCCTCACTC	GGGAAGTGCA
35401	AGGGGTCAGG	GAGTTCCCTT	TCCTAGTCAA	AGAAAGGGGT	GACAGATGGC
35451	ACCTGGA AAA	TGGGTCACCT	CCCACCTGAA	TACTGCACCT	TTCTGACGGG
35501	CTTAAAAAAT	GGCGCACCAG	GAGATTATAT	CCTGCACCTG	GCTCGGAGGG
35551	TCCTACACCC	ACGGAGTCTC	GCTGATTGCT	AGCACAGCAG	TCTGAGATCA
35601	AACTGCAAGG	CGGCGGCGAG	GCTGGGGGAG	GGGCACCCGC	CATTGCCCAG
35651	GCTTGCTTAG	GTAACAAAG	CAGCCGGGAA	GCTCAAATG	GGTGGAGCCC
35701	ACCACAGCTC	AAGGAGCCCT	GCCTGCCTCT	AAGGCTCCA	CCTCTGGGGG
35751	CAGGGCACAG	ACAAACAAAA	AGACAGCAGT	AACCTCTGCA	GACTTAAATG
35801	TCCCTGTCTG	ACAGCTTTGA	AGAGAGCAGT	GGTTCTCCCA	GCACGCAGCT
35851	GGAGATCTGA	GAACGGGCAG	ACTGCCTCCT	CAAGTGGGTC	CCTGACCCCT
35901	GACGCCCCGAG	CAGCETAACCT	GGGAGGCACC	CCCCAGCAGG	GGCACACTGA
35951	CACCTCACAC	AGCCGGTTAC	TCCAACAGAC	CTGCAGCTGA	GGGTCCTGTC
36001	TGTTAGAAGG	AAAACATAACA	AACAGAAAGG	ACATCCACAC	CAAAAACCCA
36051	TCTGTACATC	ACCATCATCA	AAGACCAAAA	GTAGATAAAA	CCACAAAGAT
36101	GGGGA AAAA	CAGAGCAGAA	AAACTGGAAA	CTCTAAAAAG	CAGAGTGCCT
36151	CTCCTCCTCC	AAAGGAACGC	TGTTCTCAC	CAGCAACGGA	ACAAAGCTGG
36201	ATGGAGAATG	ACTCTGACGA	GCTGAGAGAA	GGCTTCAGAC	GATCAAATTA
36251	CTCTGAGCTA	TGGGAGGACA	TTCAAACCAA	AGGCAAAGAA	GTTGAAAACCT
36301	TTGAAAAAAA	TGTAGAAGAA	TGTATAACTA	GAATAACCAA	TACAGAGAAG
36351	TGCTTAAAGG	AGCTGATGGA	GCTGAAAAACC	AAGGCTCGAG	AACTACATGA
36401	AGAATGCAGA	AGCCTCAGGA	GCTGATGCGA	TCAACTGGAA	GAAAGGGTAT
36451	CAGCGATGGA	AGATGAAATG	AATGAAATGA	AGCGAGAAGG	GAAGTTTAGA
36501	GAAAAAAGAA	TAAAAAGAAA	CGAGCAAAGC	CTCCAAGAAA	TATGGGACTA
36551	TGTGAAAAGA	CCAAATCTAT	GTCTGATTGG	TGTACCTGAA	AGTGACGGGG
36601	AGAATGGAAC	CAAGTTGGAA	AACACTCTGC	AGGATATTAT	CCAGGAGAAC
36651	TTCCCCAATC	TAGCAAGGCA	GGCCAACATT	CAGATTCAAG	AAATACAGAG
36701	AACGCCACAA	AGATACTCCT	TGAGAAGAGC	AACTCCAAGA	CACATAATTG
36751	TCAGATTAC	CAAAGTTGAA	ATGAAGGAAA	AAATGTTAAG	GGCAGCCAGA
36801	GAGAAAGGTC	GGGTTACCTT	CAATGGAAG	CCCATCAGAC	TAACAGCGGA
36851	TCTCTTGCCA	GAAACTCTAC	AAACCAGAAG	AGAGTGGGGG	CCAATATTCA
36901	ACATTCTTAA	AGAAAAAGAA	TTTCAACCCA	GAATTTCTATA	TCCAGCCAAA
36951	CTAAGCTTCA	TAAGTGAAGG	AGAAATAAAA	TCCTTTACAG	ACAAGCAAAT
37001	GCTGAGAGAT	TTTGTACCA	CCAGGCCTGC	CCTAAAAGAG	TTCTGAAGG
37051	AAGTGCTTAA	CTTGGAAGG	AACAATCAGT	ACCAGCCGCT	GCAAAATCAT
37101	GCCAAAATGT	AAAGACCGTC	GAGACTAGGA	AGAAACTGCA	TTAACAAACG
37151	AGCAAAATAA	CCAGCTAACA	TCATAATGAC	AGGATCAAAT	TCACACATAA
37201	CAATATTAAC	TTTAAATGTA	AATGGACTAA	ATGCTCCAAT	TGAAAGACAC
37251	AGACTGGCAA	ATTGGATACA	GAGTCAAGAC	CCATCAGTGT	GCTGTATTAA
37301	GGAAACCCAT	CTCACATGTA	GAGACACACA	TAGGCTCAA	ATAAAAGGAT
37351	GGAGGAAGAT	CTACCAAGCA	AATGGAAAAAC	AAAAAAGAC	AGGGGTTGCA
37401	ATCCTAGTCT	CTGATAAAAC	AGACTTTAAA	CCAACAAAGA	TCAGAAGAGA
37451	CAAAGAAGGC	CATTACATAA	TGGTAAAGGG	ATCAATTCAA	CAAGAAGAGC
37501	TAACTATCCT	AAATATATAT	GCACCAATA	CAGGAGCACC	CAGATTCTATA
37551	AAGCAAGTCC	TGAGTGACCT	ACAAAGAGAC	TTAAACTCCC	ACACATTAAT
37601	AATGGGAGAC	TTTCACACCC	CACTGTCAAC	ATTAGACAGA	CCAATGAGAC
37651	AGAAAGTCAA	CAAGGATACC	CAGGAATTGA	ACTCAGCTCT	GCACCAAGCA

FIGURE 3M

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37701 GACCTAATAC ACATCTACAG AACTCTGCAC CCCAAATCAA CAGAATATAC
37751 ATTTTTTTTCA GCACCACACC ACGGCTATT CAAAATTGAC CACATACTTG
37801 GAAGTAAAGC ACTCCTCACC AAATGTAAAA GAACAGAAAT TATAGCAAAC
37851 TATCTCTCAG ACCACAGTGC AATCAAAC TAACAGGA TTAAGAATCT
37901 CACTCAAAAC CGCTCAACTA CATGGAACT GAACAACCTG CTCCTGAATG
37951 ACTACTGGGT ACATAACGAA ATGAAGGCAG AAATAAAGAC GCTCTTTGAA
38001 ACCAACAAAG ACAAAGACAC AACATACCAG AATCTCTGGG ACGCATTCAA
38051 AGCAGTGTGT AGAGGGAAAT TTATAGCACT AAATGCCAC AAGAGAAAGC
38101 AGGAAAGATC CAAAATTGAC ACCCTAACAT CACAATTAAA AGAACTAGAA
38151 AAGCAAGAGC AAACACATT AAAAGCTAGC AGAAGGCAAG AAATAACTAA
38201 AATCAGAGCA GAACTGAAG AAATAGAGAC ACAAAAAACC CTTCAAAAAA
38251 TTAATGAATC CAGGAGCTGG TTGTTTTTGA AAGGATCAAC AAAATTGATA
38301 GACCGCTAGC AAGACTAATA AAGAAAAAAA GAGAGAAGAA TCAAATAGAC
38351 ACAATAAAAA ATGATAAAGG GGATATCACC ACCAATCCCA CAGAAATACA
38401 AACTACCATC AGAGAATACT ACAAACACCT CTATGCAAAT AAAGTAGAAA
38451 ATCTAGAAGA AATGGATAAA TTCCTCGACA CACACACCT CCCAAGACTA
38501 AACCAGGAAG AAGTTGAATT TCTGAATAGA CCAATAACAG GATCTGAAAT
38551 TGTGGCAATA ATCAATAGCT TACCAACCAA AAAGAGTCCA GGACCAGATG
38601 GATTCAAGC CGAATTCTAC CAGAGGTACA AGGAGGAACT GGTACCATTG
38651 CTTCTGAAAC TATTCCAATC AATAGAAAAA GAGGGAATCC TCCCTAACTC
38701 ATTTTATGAG GCCAGCATCA TCCTGATACC AAAGCCAGGC AGAGACACAA
38751 CAAAAAAGA GAATTTTGA CCAATATCCT TGATGAACAT TGATGCAAAA
38801 ATCTCAATA AAATACTGGC AAAGTGAATC CAGCAGCACA TCAAAAAGCT
38851 TATCCACCAT GATCAAGTGG GCTTCATCCC TGGGATGCAA GGCTGGTTCA
38901 ATATACGCAA ATCAGTAAAT GTAATCCAGC ATATAAACAG AACCAAAGAC
38951 AAAAACCACA TGATTATCTC AATAGATGCA GAAAAAGCCT TTGACAAAAT
39001 TCAACAACAC TTCATGCTAA AAAGTTTCAA TAAATTAGGT ATTGATGGGA
39051 TGTATCTCAA AATAATAACA GCTATCTATG ACAAACCCAC AGCCAATATC
39101 ATACTGACTG GGTAAAAACT GGAAGCATT CTTTGAAGA CTGGCACAAG
39151 ACAGGGATGC CCTCTCTCAC CACTCCTATT CGACATAGTG TTGGAAGTTC
39201 TGGCCAGGGC AGTTAGGCAG GAGAAGGAAA TAAAGGGTAT TCAATTAGGA
39251 AAAGAGGAAG TCAAATTGTC CCTGTTTGCA GACGACATGA TTGTATATCT
39301 AGAAAAACCC ATTGTCTCAG CCCAAATCT CCTTAAGCTG ATAAGCAACT
39351 TCAGCAAAGT CTCAGGATAC AAAATCAATG TACAAAAATC ACAAGCATTG
39401 TTATACACCA GCAACAGACA GAGAGCCAAA TCATGAGTGA ACTCCCGTTC
39451 ACAATTGCTA CAAAGAGAAT AAAATACCTA GGAATCCAAC TTACAAGGGA
39501 TGTGAAGGAC CTCTTCAAGG AGAACTGCAA ACCACTGCTT AATGAAATAA
39551 AAGAGGATAC AAACAAATGG AAGAACATTC CATGCTCATG GGTAGGAAGA
39601 ATCAGTATCG TGAAAATGGC CATACTGCCC AAGGCAATTT ACAGATTCAA
39651 TGCCATCCCC ATCAAGCTAC CAATGACTTT CTTACAGAA TTGGAAAAAA
39701 CTACTTTAAA GTTCATATGG AACCACAAAA GAGCCCGCAT TGCCAAGTCA
39751 ATCCTAAGCC AAAAGAACA AGCTGGAGGC ATCATGCTAC CTGACTTCAA
39801 ACTATACTAC AAGGCTACAG TAACCAAACC AGCATGGTAC TGGTACCAAA
39851 ACAGAGATAT AGACCAATGG AACAGAACAG AGCCCTCAGA AATAACGCCG
39901 CACATCTACA ACTATCTGAT CTTTGACAAA CCTGAGAAAA ACAAGCAATG
39951 GGGAAAGGAT TCCCTATTTA ATAAATGGTG CTGGGAAAAA TGGCTAGCCA
40001 TATGTAGAAA GCTGAAACTG GATCCCTTCC TTACACCTTA TACAAAAATC
40051 AATTCAAGAT GGATTAAAGA CTTAACGTT AGACCTAAAA CCATAAAACC
40101 CCTAGAAGAA AACCTAGGCA TTACCATTCG GGACATAGGC ATGGGCAAGG
40151 ACTTCATGTC TAAAACACCA AAAGCAATGG CAACAAAAGC CAAAATTGAC
40201 AAATGGGATC TAATTAAACT AAAGAGCTTC TGCACAGCAA AAGAACTAC
40251 TATCAGAGTG AACAGGCAAC CTCCAAATG GGAGAAAATT TTTGCAACCT
40301 ACTCATCTGA CAAAGGGCTA ATATCCAGAA TCTACAATGA ACTCAAACAA
40351 ATTTACAAGA AAAAAACAA ACAACCCTAT CAAAAAGTGG GTGAAGGACA
40401 TGAACAGACA CTTCTCGAAA GAAGACATTT ATGCAGCCAA AAAACACATG
40451 AAAAAATGCT CACCATCACT GGCCATCAGA GAAATGCAAA TCAAAACCAC
40501 AATGAGATAC CATCTCACAC CAGTTAGAAT GGCAATCATT AAAAAGTCAG
40551 GAAACAACAG GTGCTGGAGA GGATGTGGAG AAATAGGAAC ACTTTTACAC

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FIGURE 3N

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40601 TGTGTGGTGGG ACTGTAAACT AGTTCAACCC TTGTGGAAGT CAGTGTGGCA
40651 ATTCCTCAGG GATCTAGAAC TAGAAATATC ATTTGACCCA GCCATCCCAT
40701 TACTGGGTAT ATACCCAAAG GACTATAAAT CATGCTGCTA TAAAGACACA
40751 TGCACATGTA TGTTTATTGT GGCACTATTG ACAATAGCAA AGACTTGGAA
40801 CCAAGCCAAA TGTCCAACAA TGATAGACTG GATTAAGAAA ATGTGGCACA
40851 TTTACACCAT GGAATACTAT GCAGCCATAA AAGATGAGTT CATGTCCTTT
40901 GTAGGGACAT GGATGAAATT GGAAATCATC ATTCTCAGTA AACTATCACA
40951 AGAACAAAAA ACCAAACACC GCATATTCTC ACTCATAGGT GGAATTGAA
41001 CAGTGAGAAC ACATGGACAC AGGAAGGGGA ACATCACACT CTGGGGACTG
41051 TTGTGGGGTG GGGGGAGGGG GAGGGATGGC ATTGGGAGAT ATACCTAATG
41101 CTAGATGACG AGTTAGTGGG TGCAGCGCAC CAGCAAGGCA CATGTATACA
41151 TATGTAACCTA ACCTGCACAT TGTGCACATG TACCCTAAAA CTTAAAGTAT
41201 AATAATAAAA AAAAAAGACT CAAAGGCACA GTCCTGACA GTTTGATTTT
41251 TTATAATAGC TGTTAATTTT CCTAACTTCG AGGAAGTTGA TAGCATGTTT
41301 TGAGTATATT TCAAACTAC ATTCAAATGT TGCAATAGAA CATTAGAAT
41351 TATCTTCATG ATCCACTAAG TGCATGAAAA AAATGGATAA TGAATCTATT
41401 CATTACCATC GTTTAATATT TTATCTTCAA GTTTTGTGT TTTGTAGCTC
41451 ATTGGCAGAG TTTGACGAG TGCTGAAAGT ATTCTTTAGT GAGCTGGCTG
41501 TAATTTTTGG GCCCATTTTT ATCTAGATAA TTAAACTAT CTGACAGGAC
41551 CATAAAATGC TTGCTGCCAT TTCCAACAAC CTATATTTGT GGATGGGGTT
41601 TTTTAATTTA ATGAGAATAT TATGTTAGAA AAGAACTGT CATTCTGTAA
41651 AGTGGCCAAT AATGTTAGTT TTATTTATCA ATTTAGTTT GTACTTTGAT
41701 CATTTTTTTA AAATTTTCAGC ATTGATGTTG ATGGGACAAT GACAGTGGAC
41751 TGGAAATGAAT GGAGAGACTA CTCTTTATTT AATCCTGTTA CAGACATTGA
41801 GGAAATTATC CGTTTCTGGA AACATTCTAC AGTAAGTCTA CTTTATGTAT
41851 TTATACTTAT TTGGAGCTAT AAACCATAGG TACAGTTATC ACCCAAGAAC
41901 ACTCTGTAAC ACTTATGGGC CAGGATACCT GAGTCCCAGT AGCTCCTTAA
41951 CCTGTAGAGT TCTATTTATT CTATTAGGCA TAGATTTATA GAGTATTAAA
42001 CAAAAAAAAA CAGCTCTCCC TCTCCCTCTC CCTCTCTCTC CCCCTCCCCA
42051 CGGTCTCCCT CTCCCTCTCT TTCCACGGTC TCCCTCTGAT GCCGAGCCAA
42101 AGCTGGACTG TACTGCTGCC ATCTCGGCTC ACTGCAACCT CCCTGCCTGA
42151 TTCTCCTGCC TCAGCCTGCC GAGTGCCTGC GATTGCAGGC GCGCACCGCC
42201 ACGCCTGACT GTTTTTCGTA TTTTTTTGGT GGAGACGGGG TTTCGCTATG
42251 TTGGCCGGGC TGGTCTCCAG CTCCTGACCG CGAGTGATCC ACCAGCCTCG
42301 GCCTCCCGAG GTGCTGGGAT TGCAGACGGA GTCTCGTTCA CTCAGTGCTC
42351 AATGGTGCCC AGGCTGGGGT GCAGTGGCAT GATCTCGGCT CGCTACAACC
42401 TCCACCTCCC AGCCGCCTGC CTTGGCCTCC CAAAGTGCCA AGATTGCAGC
42451 CTCTGCCCAG CCGCCACCCC GTCTGGGAAG TGAGGAGCGT CTCTGCCTGG
42501 CCGCCCATCG TCTGGGATAT GAGGAGCCCC TCTGCCCTGGC TGCCCAGTCT
42551 GGAAAGTGAG GAGTGTCTCT GCCCGGCCGC CATCCTGTCT AGGAAGTGAG
42601 CGTCTCTGCC CGGCCGCCCA TCGTCTGGGA TGTGAGGAGC CCCTCTGCCT
42651 GGCTGCCCAG TCTGGAAGT GAGGAGCGCC TCTTCCCGGC CGCCATCCCA
42701 TCTAGGAAGT GAGGAGCGTC TCTGCCCGGC CGCCATCGT CTGAGATGTG
42751 GGGAGCGCCT CTGCCCCGCC GCCCGTCTG GGATGTGAGG AGCGCCTCTG
42801 CTCGGCCGCC CCGTCTGAGA AGTGAGGAGA CCCTCCGCCC GGCAGCCGCC
42851 CCGTCTGGGA AGTGAGGAGC GTCTCCGCC GGCAGCCACC CTGTCCGGGA
42901 GGGAGGTGGA GGGGTGAGCC CCCC GCCCGG CCAGCCACCC CATCCGGGAG
42951 GTGAGGGGTG CCTCTGCCCC GCCGCCCCTA CAGGGAAGTG AGGAGCCCCT
43001 CTGCCCGGCC ACCACCCCAT CTGGGAGGTG TACCCAACAG CTCATTGAGA
43051 ACGGGCCATG ATGACAATGG CGTTTTTGTG GAATAGAAAA AGGGGAGAGG
43101 TGGGGAAAAG ATTGAGAAAT CGGATGGTTG CTGTGTCTGT GTAGAAAGAG
43151 GTAGACATGG GAGACTTTTC ATTTTGTCT GACTAAGAA AAATCTTCT
43201 GCCTTGGGAT CCTGTGTATC TATGACCTTA CCCCCAACCC TGTGCTCTCT
43251 GAAACATGTG CTGTGTCCAC TCAGGGTTAA ATGGATTAA GCGGTGCAA
43301 GATGTGCTTT GCTAAACAGA TGCTTGAAGG CAGCAGGCTC GTTAAGAGTC
43351 ATCACCCTC CTAATCTCA AGTACCCAGG GACACAAACA CTGCGGAAGG
43401 CCGCAGGGTC CTCTGCCTAG GAAAACCAGA GACCTTTGTT CACTTGTTTA
43451 TCTGCTGACC TTCCCTCCAC TATTGTCCTG TGACCCTGCC AAATCCCCCT

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FIGURE 30

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43501 CTGCGAGAAA CACCCAAGAA TGATCAATTA AAAAAAAAAA AAAAAAACA
43551 ACCCAAGACT GCATAAATGT CCATTCTGAA AACTTGGAAG AAGTACCACC
43601 TTGATGAATA AGCTGTCTAG CTTTATTGG CATTTAAGTA TTCTGCCATA
43651 GGGAAAGTGA AAAGTTGTAG GCTTTTACTT TTTATAGGTA CTATATTGTC
43701 CAAATAATCT CAGCACCTCA TGGTTGCTAA GGATCTGTGT CCTTGTTTGG
43751 TCAGATTATG TTTATCTCTG GCATAAGGCA CTTAACAATA TTCATTAAAG
43801 GTTACAGAA CTTTTGTCTT CATCTGCTTA GCATTTTATA CCAGTTTGT
43851 TTCCACCAAA CTTTCAAAT TTGATTGTTT CATTAAATATT CTGCATACTG
43901 ATGTAAACCA AGTTCTATTA TTGTGCAATC TGCTCCTGAA ACCCTTAGGA
43951 ACTCTCTGAA GGAGTTTTAT TTATTTTTTG TTTTGTTTT TGTTTTTGT
44001 TTGTTTTTTT GAGACGGAGT CTTGCTCTGT TGCCCAGGCT AGAGTGCAGT
44051 GGTGCGATCT CGGCTCTCTG CAAACTCGGC CTCCGGGGTT CACGCCATT
44101 TCCTGCCTCA GCCACCGGAG TAGCTGGGAC TACAGGCACC CACCACTGCG
44151 CCTGGCTAAT TTTTTTGTG TTTTGTAGT AGACGGGGTT TCACCGTGT
44201 AGCCAGGATG GTCTCGATCT CCTGACCTTG TAATCCGCCC GCCTCGCCTC
44251 CCAAAGTGCT GGGATTACAG GCGTGAGCCA CTGTGCCCGG CCTTTTTTTT
44301 TTTTTTTTCT TTATGGGCTT GTCTTCTACA CTTTCAATTT GACTAAATTA
44351 AATATGCATT AAATGAAGTC AGGAGTTTAC ATTGCCACTA GTAACAATGC
44401 CTAAGCTTAC ATAAAGCATT ATAAATTTGT TGGTGATTAG TGCCTTCTCA
44451 GCTATGAGTA TAAGATAATA TTATACTAGT AGTTTCAAGTT CCTAGATAAA
44501 TTGTACACTA TGTGAAGTTT TATTTACATA ATTCTTACGG TATTTTTTAA
44551 GGTAGTTGAT AACAGTTGAG ACTACAATTG TATCTCCATT TTATTGATAG
44601 TAAAATGAAG GAAGGGAGGG TTAAGTACAT AGGAGAGCTC CTCCCCGTTG
44651 CACTCTTGCC TGTAAAAATT TTCTTGCCAA AACAATTTAG ATAATAGAAT
44701 TGTAAAAATA TTATTATAGA ATTGTTTCTC TCAAACATA GTAATGTAGA
44751 ATAGGTTGAA GGGGTGATGA TTTGAAACAA TACCTCTCCA TTAGCTAAAT
44801 TTTATATAGA ATCTATTGCA TGTTTTAAAT GATAAGTCAG ATTTATAAAA
44851 ATATTTTTAT AAACAGTAGG AAATGAGTTT AGGGGTATTC ACATACAGTT
44901 TTAATTTTTA TTTACATATT TAAAAATAT CATGGTATAA ATATGATGTG
44951 GATATAAATT TGAGATAAAG GAAGTATTGT TTAAGAAATT ATGAACTAAT
45001 TTCTTAAAG ATGTCATCAC CAGTTGGTTT TCTAGCCTTA TGAAAAATGG
45051 TTGCAATAAA AAAGATTGAC TATGATAAAA TGCTGCCCTT TCATTTTAAC
45101 CTAGACCAAG AGAAAACATA CTGTGAATCT ATGATGAATG AAAGAAAGTT
45151 GTAAGTGTG GTTTTGTATA TTTGTAATTA CTGTTTATT TCATTTCTG
45201 TGAAGTATA CTGTACTTTG TTCATTGTGA GTAGACAAC TATAATCTAT
45251 GTAAGTAAAT TGGTTTAGTA TAAATCTAG GGAATGAAGT TCATATTAAC
45301 TGTAAAAATA CATGATTGTT CTCTAAAACA AAACGTCCTC TGGGATTATT
45351 TTTAACTAAG GCGCATGGGG ATCTTTTTTT CATTTTACA GGAATTGAC
45401 ATAGGGGATA GCTTAACTAT TCCAGATGAA TTCACGGAAG ACGAAAAAAA
45451 ATCCGGACAA TGGTGGAGGC AGCTTTTGGC AGGAGGCATT GCTGGTGTG
45501 TCTCTGAAC AAGCACTGCC CCTTTGGACC GTCTGAAAT CATGATGCAG
45551 GTGAGCTTTA TTATCGTGTG TCCAGGTTTG CCTAAAATAT TCTAAAACAA
45601 TGAGAAATGT GGTGCTTTGA AAAAGAAGTT TTAATTTTCT TCAGTAATAA
45651 TCTTTTATAC CCTAAAAAAT AAATCTATT TGTGCTGTT AACTCTAAAT
45701 TCAGTCCATG TAAGTATGGC AGTGTACCAA ACCTTAAATT GTTAGTACAT
45751 GTGTGAATG AACTTTTAAT CTTTGGCATT CTATGACTAT TCAAACATTT
45801 AATTCAAAAA ATATCTCTAG CTATTGTTGT AGGATTCTCC TGATTTATAG
45851 TTTCTTCTT TTTAATATAC TTTATCAAAA GTAAAGTATT TTTGAAATCT
45901 AGACTCTTAG AGCAGCAATG TAATTTTGAA AATTATTCTA AAGCTGAGGT
45951 TAGCAGAAAA AGATCTGGCT TTATAGACTG ACTTTGCTAT TTAGTAGCAG
46001 TGTAGCATTG GGCTGGCCAG AGTGGAAGA GGAATGGAA AAGAATTAAT
46051 ATGTATTTGC TCATCTGTGT AACCCAGTTA ATCCTTGAC CAGCCAGTG
46101 AAGTAGGAT TTTATCATTT TTCCAGGGGG AATCTGAGGC CCAGAGAATT
46151 GACTTTTCTT TTACAACAAA TGAGAGGGGG AATGAGTAT CTTTGCCTCC
46201 AGTGCTCCTG GTTCTCATGC TGCATGAAAC CTCTGAGGTC TCATTTTCTT
46251 TCATTCTGGG ATGGGGATAA GAATATCTAA TAAGAATGGT TTAAGAATCA
46301 AGCAATATCA GGTATGTGAT AATGTCTGGT AACTGGAAT AACCTATTGG
46351 AACATAGTAG TTGTTTACAA AATATTTTAA AACTTTGTT ATACTTATGG

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FIGURE 3P

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46401 TCAACACTTT TTATATTTGT CTGTAGATTT CTGTACAAAA AGATTCTGAC
46451 ACTGTTTTAA GCCAGCATTG CTTCAGAATG TACCCAAATC TCAAAATTTA
46501 TTTAGGGGCA AAGCTAATGC TTTAAAGAAA AAGGAGAGGG GATTGGTGTG
46551 TGTTTTCTT TAGGAACAGT AGTAACTTGA CTTTTAGAGA ACTTGAATAA
46601 GCATTTATTT TTTCTTTTGT CCTATTTTAT TGTGAAGTTT ATTTATTTAA
46651 AATAAAATGG ATTTCTCTGG AATTTAGTTT CTGCAAATTT GAGGAGTTTC
46701 CAAAGTCAAC CTTCAGGTTT GATACTTCTC TAGAAAGACT CACATAACTC
46751 ACTGAAAGCT TATTACCCCT GGTATGTTT TATTACGGGG AAAAGATGCG
46801 GATGAAATC AGTCAAGTAA AGAAGCACAT AGGGCAGAGC TTCTGTTGTC
46851 CTCTCCCTGT GGAGTCTCCA TGTCTTACTT TCCTGGCACT GTTATGTGGC
46901 ACTAGGCATG GAATATTGCA GACCAACCAG GGAAGCTCAC CTGAGCCTTT
46951 GGTGTGCAGA GTTCTTATTG GGGCCTGTTT TCATACTGGC CACATGGCTG
47001 GCCTTCAGAA TTCAACCCGT TCTGTGAGTG TGTGTGTGTG TGTGTGTGTG
47051 TGTGTGTGTG TGTTTAGTGG TAGTCACCCC TTTTATGTGA GCTGAAACAA
47101 TCAGAAGAA AGCTGATTTG TTTAATTATT TTTGGTGTAT TGGACTTAAT
47151 CAGTTTTTAT CTGTAGGTGG TCATAAGGTA CAGTATTTTT AAGTGACTAC
47201 CACATCTGTA GTATAAGCCA AGTAATTTAT CAGTACTCAC AGGATGGGTA
47251 CATGTTGTAA TGAATTTATT GCCTAGAGAG GGCCTCAAAA TATGCCAAAG
47301 AGGGTGCAAT TTTTATTTTT GGTTCAGGC TGTATGCATT CCAGTGTGGG
47351 TAGCCCTGAT ATACACAATA TCCAAACCAT TTCAGACCCA TTTACAGTTC
47401 ATGTCTGTAC TACTTCTTGA GGAGAGGGAG TAACATATTA CTTTAAATTA
47451 TATGTAATAA TATACATACA TTAAATTATA TGTAATAATA TAATATTATT
47501 ATTTGCAGTA TACTTTTTTA TTTCCCTTTA ACTGAGCTTG TTCATGTTTC
47551 AAAGGGTGTT CCATTGCCTG ATACATAATT TAGTTAATAT TATCTTATGA
47601 AGGTTGTTCA TAATTTTAAT ACTCTTCTTG TCTTCTCTCT CTGCTTTCTC
47651 AACTGAAGA TACCAATTAT TCTTAGTTTT AGAGTCAGAG ACAGGCCTCT
47701 AAAATCATGG CAATACTCCC TCTCATCATT ATATATATTT TTCAACCTTT
47751 CTATATTTTA TTTTCAAATA TATCTTCTTG CAGTTAGAAA CGGTATTGAA
47801 AAAGATTGTG TGGTTGTTCT AGAAAAAGTA ATAGTAATAT GCCACCAGCA
47851 TTTTATATCA TTCTGCTTTT ATTTTTFAGG TCACGGTTCA AAATCAGACA
47901 AAATGAACAT ATTTGGTGGC TTTTCGACAGA TGGTAAAAGA AGGAGGTATC
47951 CGCTCGCTTT GGAGGGGAAA TGGTACAAAC GTCATCAAAA TTGCTCCTGA
48001 GACAGCTGTT AAATTCTGGG CATATGAACA GGTAATTGTT ATCACCCGTG
48051 GAATTTATTA ACAAAGAGGA GTTAGTAAAC GGATTCAATA AATGTTAATG
48101 TATAATGCTT TTGGGATTCT TGTTTAAATA CATGATAATC TTTACATAT
48151 ACCCCATAAG GAGGATCACT TATAGGAGAT TAGACTAAAT AAAATCAGAG
48201 ATTTCTCATG ACCAAGTTAT GGGATTCTTA ATTCATCATA TTATTTATAA
48251 AGTTTTTTTT TTCTAAGTAG TTCTTAAAGG AAGGGTAGAA TTTTAGTTTA
48301 TTCATTCTGA ATCCTGAGCA GAAGCAGCAC ACTAACATAA GTTTTATGAA
48351 AGTGTACAAA TCTAACCTCT GGAAGGAAAA CTATAAGTTG AAGTCCTTTG
48401 TGTAATTTGA CGTTGCTGTA AAATTGAGCT GAGTTTGGAG TGACACCTCC
48451 ATGAAGGCAG GGGCGTGGCT TCTTCCCAT GTACTCCAGC ACCTAGACAG
48501 AGCTTGGCAT GTGATAAGTT TCAAGCGAGT GTTGAATGAG TCAATGAATG
48551 AACAAATGCA TTTACCTCTG AATCACTTCT CTGTCGGCTT TTGTAACTT
48601 GGATTATTTG AGCTATTGCT TCAGCCTAAC TCAATGTAAA GGGGAAATAC
48651 AGAGGTAAGT TTTAGAGTTT GGGTTCTCTT TATGGTCATT AGCAGAAGTG
48701 TCTAGTTGAG CAGCCACAGA TTATGTTTTT CATTATTTAT TCCATCATTG
48751 TTTATCAAGG ACTGTAAGGG CCTTGAAATT CAACTCCCCC CCCCATAGTT
48801 TTTGTATTAT TCCATGTAGA TTTTAGATTA TTCTGGAGAG TGTTTTGTTC
48851 TTGAGCAACA GAATACTCTT GAGAAGATTA CGAAGTCCAG TGGTATCCTT
48901 TTCTTTGCCT AGGAAATAGA GAAGCAAAAA AAAAAAAAAA AAAAAATTAA
48951 AGAAAACTA GTCTCCAGGA TTTTAATTAG AACCTATCCT TGGGAAGGCT
49001 ATTTTCTTTA TATGAAGTTT TGAAGATTCA AATCATGATT ATTAAGGGCT
49051 AATGTTTGAG ATACCCCTAG GTTATTCTGA CCACATACTT GGATTTTATG
49101 ATAGGAAAGC CACAGCCTAA AATAAAATAA TACTCAATGC AGTTATTTCA
49151 GTATGCAAGA AGTTTGGTAT TTTTGAAAAA GTCCATGGGT ATTGCAAGCA
49201 AATATGCACA TTTTGCTTTA TGCCATTTGT CAGATTCTTA CCTTGATAC
49251 CACCAACAGG CATCCTCTGC TTCTGTCCAC CCAAGCTCCT TCCTGAGACC

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FIGURE 3Q

49301 TCTTTATAGT ATTGTGATTT CTGCACACTA ACTTTCTTAG ACATGAAGAG
49351 AAAGCTGTCT ACACAGTGTG GTGTAGTTTT CTTATGGGCT CTGGACCTAT
49401 GGTGCTGTTT TCTCTCCTCC TGCTGAAGGT CCATTCATCC CTCGGGGCTC
49451 TCTAAAAGCC ACCTTCCTGT GACAAGCATA TACTAAGCAT CTCAATCAAA
49501 GCCAGTTCCT CCCCTGTCCA GCCTCCCTCG AGTGCTGAAT TGCAGAATAT
49551 CCCATTTTTT ATTGGATGAT GGAAAACCCA TTGTTTTCCC AGTGGATTGT
49601 AAATTACTTC GGGGTAAATA GGCTGTATAT ATTCTCAAAT TTCCCAGAGT
49651 ATGTAAGTAG GTCACTTTTA GATTCAGATA GATTTTGTTC CTTGAATAGC
49701 TAGTACTTTA GGAACTAAG AAAAAGATCT TTTCAACCTG GTATGTAGCT
49751 CTGTCAAACA CATCATCAGT ATGGGGTAAA CCTGTGTTCT CTGTGGGTTG
49801 TCATTACCAT AGTAGTGTCA TTGTATCATT GACAGTGTAA TAGTGTGGGG
49851 TAGTGTTCTT GTGGTTTCAG CTGCCACTCT GACTGACTG CTTTCCACTC
49901 CAACATCTTC CTCTTTATCT CAACACTGTA GGTCTACCTG TGTACTGTGT
49951 GTTTCAGCAT CTCTGCTTGC ATGACCCAGG AGTGCCTCCC ACTCAATATG
50001 GCCACCATGC ATGGTCATCT TTCTGCTACT CCCTGTCTCC TGACCCTGCT
50051 CCAGCAACAC AGACAGACAC CCTTCCTCTT TCTATATGTC ATATGGTGGG
50101 GAATGCCCTT TAGTACTTAC TCAGGAGTTA GTTCCTCTGG GAAGCCTTCT
50151 GTTCTAGTTT CTTTTTGTGA CAGCACTTTC ACATTGAATT CTGACGTTCT
50201 CTGTACTTAT CTGCTTTGTG AGACTGTGAG CTTCTTAGG CAGTAGCTAC
50251 TTGTATTCTT AGCACCTTGC CCAGTGCCAG GAAACCCTTA TTAAGTAAAT
50301 GAAAAGACAG AACTGACAGA CTGGAATTAG AGCTCAAGCT TGCCTCAATC
50351 TCAAGCCATT AAGATGAAGG GGAGCCGGGC GTGGTGGCTC ACGCCTCTAA
50401 TCCCAGCACT TTAGGAGGTA GTTTGCTTGA GCCCAGGAGT TCAAGACCAG
50451 CCTGGGCAAC GTGGCAAAAC CCCATTTCCT CAAAAAATAT AAAAATTAGT
50501 TGGACGTGGG GGTGTGTGCC TGTACTCAGG ATGCTGAGGT GGGAGGATCA
50551 CTTGAGCTCG AGAGGCAGAG GTTGCAGTGA GCTGGGATCA CACCATTGCA
50601 ATCTAGCCTG GGTGATAGAA TGAGACCTTG TCTCAAAAA AAAATAAATA
50651 AATAAAATAA GGGGAAGATA AGGATTGGAA ACAGAAGGAG CAGCATGTGG
50701 ACAGAAATGT AGGCACAAGA AGGCATCACT CACTGAAGAG ACTGAAAGTG
50751 GTTCACTGTG CCTCAAGACT GGTGGAGTGT GTTCCGGAA AGATAATGAT
50801 GAAAGAGCTG CAGAGATAAA CAGGGGCCAA ATGTAATAGG AGTCTGGATT
50851 TTATTCTGAA TATGGTAGGG GCTATTGTAG CATCTTATAT AGGGAAGTGA
50901 AATGAGTACA TTCACATTTA AGGAATATCA ACCTGAAAAA AGAGTGGAGA
50951 CATTGTTGGG GGAGAGTGAG GTAGACTAGA GGCAGGGAGA ATATTTAAAT
51001 AATTGAGGTA AGAAATGATG AACACCAGTA TAAGGTGATG TCTTTAAGGA
51051 ATGGAGAAGG GAATGAACTG AGAAATATTT TGGAAGTAGA ATCAACAGAA
51101 CTCACTGACT GACTGGATAT GGAGGTGAGA AAGAGAAGAG TCAAGAATGA
51151 TATTCTAATT TCTAACTTGA GTGACTGCAT TCAAAGAGAA TACAATATCA
51201 GGTTCATT TTGTGCATGCT GAGTTTGAGA TGTGTGGGAC ATGTACAGGG
51251 AGCTGTCCAG TAAGCAATTG GGTATATCAG CTAGCCATTA AGAGAGAGAT
51301 CTTTGATAGA GAGGTTGTTG CTGAGTTGAG CCATTGGAAT GGGCAGGATC
51351 ACTCAAGAAG AGCTTATAAA TGAGAAGAAT TCTAGGAATA AGTCCAAGG
51401 GAGAAGTAAA AGAAGAACT TGCAAAGGAC ACTGAGAAGA AATAGCTCGA
51451 GGGATGGGAG AAAATCCAGA GAGAGGGATG GCATAGGAGT CAGTGGAAGG
51501 AAACGGTTTC ATGGGGGTCA GTACTACTGG GTAGTGAATA TAATAAGAAT
51551 ATCTTTTAGG ATTTCTCAAC CCAGAGATAG GTAAGCTTAG TATAAATGCT
51601 TCTGTGAAGT AATGAAATGA GAAACCATGC TGAAATGAGC TTAAAGTGAA
51651 TGGGAGGTGA AGAACTTGG ACAGTAGAGA CACATTTTTA GGGAGTTTGA
51701 CAGTGAAGAG AAGGAACTA GAAGAGGGAG AGGGTGATAG ATAAGAAAGA
51751 TGTTGGGTGG AGGGGATTTG TTTTTTGT TTTTGT TTTTCTGTTT
51801 GTATGTTTGT TTGTTTTTGA GATGGAGTCT CACTTTATCA CCCAGGCTGG
51851 AGTAAAGTGG TGCAATCTCA TCTCACTGCA ACCTCTGCCT CCTAGGTTCA
51901 AGTGATTCTT CTGCCTCAAC CTCCTGAGTA GTTNNNNNNN NNNNNNNNNN
51951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
52001 NNNNNNNNNN NNNNNNNNNN NNNNTGCCT CAGCCTCCCG AAATGCTGGG
52051 ATTGCAGGAG TGAGCCCCC GTGCCTGGCC TGGAGGGAGG ATTTTGATTT
52101 GACTTTAATG TGCCTGTTGC TGAAGGAAGC ATGTCAATAC AAATAAGAA
52151 GTTGAACA TAGGTAAGAG AGGTTGATTA ACCCGGTAGG TGTTTCAAGG

FIGURE 3R


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52201 GAGTTTGTGT GTAGGGAAAG GGAGTGGGAG ATGGAAAGGG GCTGGGGGAG
52251 ACAGGTTCTA TCCAGAGACT GTTAAAAGGA TTAGTCTTTG ATTACAAGAA
52301 GAACCTTTCT TATACGTGTT TGGGAAGAAA AAATATGTGA GTAGCTATGG
52351 ATAATTTTGC AGGAGGTGGG CAGAATACCA AGATATTCTG CCTGGTGGCC
52401 TCTCTACTCT TCCTTGAGCT CCTGAGAAAG GATGTGATCT GAGAATGAGG
52451 GAGGAAGTGG TATTGGAAGC TGGAGGAGAA TGGAGAAGAT CAAAATGGTT
52501 AGTCTAACAA ATGGGAGAGA ACTGAGATAG ACAAAGGAT TTCAGGGTGG
52551 TTTTGAGGGC TCAGTTAAGT CTCCTTTAGG AAGGTTCACT TCTGTAGCCT
52601 TGGCAAGTTA CTTAAAGTCT CTGTGACTAT TACCTCATCT CTAAGATGGG
52651 GACTAAGCTT GGTGACATAG TTTTACATAC CAGGCACAGT GCCTGACTTT
52701 TTGGCTCTGT CCTGAAGTCT TCCCTTTGTA TATGGTATGT TTCGGGGAAT
52751 AGGAGCCTCA AGCACTTATC CTTTAAATAT TTATCCTCCA TCAGTCACTA
52801 AACGTTTACT CTGTACTTTT GATAGGTGCT GTGGGGGTCC AGGGTATAAA
52851 AGGTACCTTC AAAGTACTG TTAAGTGCA GGAAGTTTT TAAGCAAATT
52901 ATGTTTAATG ATTTTGACAA TCTGACATGC AGGAAAATTA ATAGGGCCTA
52951 TGCAGAAGAG GAGTTTTATG TAACACTCTG TAGTTCAGGA AACAGAGCCC
53001 TTGGAAGCAG TGATCTCTCT GGGGAGGAAT GTCTGGTATT TGGGAATCTC
53051 ATGAAATGAT AATATACTTA ATTTTATCA TGAGCAGCAA AACACAGATT
53101 TGCTAGGAGA AAGTCATCGT ATGTTGTTGC ATTGGGCACT TTAGATCCCA
53151 GGAACAGAA ACTGGCTGGC ACAGGAATGG GCATCACTGT GGGGATGGAT
53201 CATGTAGGGG AAGGATCCCT GGAGAAGTCC AGGAGGTGAG ACTTCCCCCT
53251 TCCCTTCTCC ATGCATGAGT CCACTTCTCT CTGTGACTT TCCCTTGTCT
53301 CCTCTGGTGA CAGCAGCTGC TTACCTCTGG AGACCCCTC ACATTCTGA
53351 GAGAAGGAAT CTGGCTTGCC TGGCTAATTC CCATGGTCTA TGTITGGGCA
53401 GAATGTCTTA GCAAGTTGTG TAAAGATAGT GTATTCATAT ATTAATAATA
53451 ATAATAACAT CTAAGTGAACA TTTGCTAGGT GTTCAGACCT GCACTAACCG
53501 TGTTACAAGT ATTATTTTTT TGTAACTCTT TCCATAACCC TGTGAGGTAA
53551 GTACTGTTAT CACAGACAAG GAAACCACAA TGTGGACCTG TTCATGAAC
53601 TGCTCGAGGC CACGTGGCTC TGGAGTTCCA GCTCAGGTCT GCCTGACTCT
53651 CAATCCCATG ATATAATAT ACTGGCCAGT CACTATTTTG GCTGTATTGG
53701 GGTCAATTTT ATACCTTGG TCCAGTTAGC TATGTTGGGT CACTTTAGTA
53751 CTGATAGCCA GGGAGATGCT GGGCTTGATA GGTAGTATA ATTCTATGTA
53801 TTACCTACAA AAAGTGTGTT TATAAATTGT TTGTTAACA TTTGTTGTCT
53851 ACCTATTTAT TCATTTTATT TGCAGTGGTG AAAATAAACT CATCTTTTAA
53901 AAAGTGTGGG GAAAATATCC AAACATTGTG AAAACTTGAT TAACCTTGTA
53951 TTTTCTGTAC ACCTGGGGAG GGATGCTGTT ATGCTGTTTC AGCAAAGGAG
54001 CAAGTGGTGC CAATCTGGGA GACATCTGTG TTTTGTGGAA ATCTGACTTG
54051 AAAACCACTG TCCAGTCACT GCGTGTATTA GCATTTAGGC CTTGCTCTTC
54101 TGCTATGTAT TATTAATGTA GTGTATACAT TCGAGACAC ATCATCACAT
54151 TTGTCAATTT ATTGATTTCT AGGAGCTGAT TTGTATTCTA GGATTGTCTA
54201 GTTGGCTTGG GCTGCCATAA AATACCACAG TGTGTGTGGA ATCAACAACG
54251 GAAATTTATT TCTAACAGTT TCAGAGGCGG GAAAGCCTAA GATCAAGGGC
54301 CAAGCCAGTT TGATTTCTAG TGAGCGTTCT CTTCTCAGCT TGTAGACAGC
54351 TGGTATGTGC TCACATGGTC TTTTCTTGGT GCACATGTGA AGGGGGAGAG
54401 AGAGAGTGGG CTCTCTGGTG TCTGCTCTTA CAAGAACTAT GATCCTGTCA
54451 TGAGGGCTCC ATCCTCATGA CCTCATAACC CTAATTACCT CCAGAAGCCT
54501 CATCTCCTAA TACCATCACA TGGGAGGTTA CAGCTTCAAC ATATGAATTT
54551 GGTGGGGGTG CAGCTCAGTC CACAGCAGGT AGTAATGTGC ATTTTAAAC
54601 TTGTTTATAC AGTACAAGAA GTTACTTACT GAAGAAGGAC AAAAAATAGG
54651 AACATTTGAG AGATTTATTT CTGGTTCCAT GGCTGGAGCA ACTGCACAGA
54701 CTTTTATATA TCCAATGGAG GTGAGTACCA TTGTCAAGTC TGAAGTGTG
54751 ATGGTGTTCG TGTTGGTTGT CTATTGCTCT CTAACAAGTT ATCCCAAAT
54801 TAACAGTTTA AAACAAGCAT TTATCATCGC ACAGTTTCTC TGGGTGAGGA
54851 ATCTGGAAGC AGTTAGCTG GGTGCCCTCT GCTCAGGGTT TTTACAGGCC
54901 CACAGTCAAG ATGGTAGTCA GAGCTTGGA TCAAGCTGGAG GCGGATTCCA
54951 AGCTCACTCA TGTGTCTGCC AGGCCTCACT GGCTATTGGC TGGAAACATC
55001 AGTTCCTTAT CACGTGAGCC TTTCTGTAGG CTGCCTGAGT ATCCTCAAAA
55051 CACAGTAGCT GGCTTCCCTA GAGTCAGTGG TCCAACAGAG AGAGAGAGAG

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FIGURE 3S

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55101 AGAGTGCCTA AGATGAAAGC TGGTATCTTT TGCCTCTTCT GCTGTATTCC
55151 ATTGATCACA CAGACCAACC CTGGTAGAGT GTAGGAGGGG CTGGTATAAT
55201 GGTGTTAATA ACCGGAGACA AATATCACTG GGGGTCACTT TAGAGGCTGG
55251 CTGCCACTTT AGAGGCTGGC TGCCATTCTT GTCCAAAGAG TTTCTGTACC
55301 ATAAATTTAA TAATGGAATC TCAGGATTGT ATTATATGGT GATTATCCTA
55351 ATTAGACATC CTTTCATTAG TGCATAGGTT GGCAAAACAC AGACCTACGG
55401 ACTGTTTCAT ACAGCCCTTG ACCTAAGAAT GCCTTTTACA TTTTAAAAAA
55451 GTGGGCAACA CAGGAAAAAG TGAGAAAGAT CTAAAATCGA CACCCTAAGA
55501 TCACAATTAA AAGAACTAGA GAAGCAAGAG CAAACAAATT CAAAAGATAG
55551 CGGAAGACAA GAAGTAGCTA AGGTCAGAGC AGAACTGAAG GAGATAGAGA
55601 CACGAAAAAC CCTTCCAAAA ATCATTGAAT CCAGGAGCTG TTTTATGAA
55651 AAGTTTAAAC AAATAGACAA CTAGCCAGAA TAATAAAGAA GAAACCAGAG
55701 GAGAATCAAA TAGCCCCAAT AAAAAATGAT AAAGGGGATA TCACCACCAA
55751 TCCCACAGAA ATACAAACTA CCATCAGGGA ATACTATAAA CACCTCTATG
55801 CAAATAAACT AGAAAACTA GAAGAAATGG ATAAATTCCT GGACACATAC
55851 ACGCTCCCAA GACTAAATCA GGAAGAAGCT GAATCCCTGT ATAGACCAAT
55901 AACATGTTCT GAAATTGAGG CAGTAATTAA TAGCCTACCA ACCAAAAAAA
55951 ACCCAGGACC AGACAGATTG ATAGCCGAAT TCTACCAGAG GTACAAAGAG
56001 GAGCTGATGC CATTCTTCTT GAAATTATTG AAACAATAGA AAAAGAGAGA
56051 TTCCTCCCTA ACTCATTTTA TGAGGGCAGC ATCATTCTGA TACTAAAACC
56101 TGGCAGAGAC ACAACCAAAA TAGAAAATTT CAGGCCAATA TCCCTGATGA
56151 ACATCAATGT GAAAATCCTC AATAAAATAC TGGCAAACCT AATGCAGCAG
56201 GACATCCAAA AGTTTATCCA CCATGATCAA GTTGGCTTCA TCCCTGGGAT
56251 GCAAGGCTGT TCAACATATG CAAATCAATA TAACGGAATT CATCAATAAA
56301 CAGAACCAGT GACAAAAACC GCATGATTAT CTCAATAGAT GCAGAAAAGG
56351 CCTTCGATAA AATTCAACAC CACTTCATGT TAAAACTCT CACTAAACTA
56401 GTTATTGATG GAATGTATAA CAAAATAATA AGAGCTGTTT ATGACAAACC
56451 CACAGCCAAT ATCATACTGA ATGGGCAAAA GCTGGAAGCA TTCCCTTTGA
56501 AAACCGGCAC AAGACAAGGA TGTCTCTGTG CAGCACTCCT ATTCAACGTA
56551 GTATTGGAAG TTCTGGCCAA GGCAATCAGG CAGGAGAAAG AAATAAAGCG
56601 TATTCAGATA TGAAAAAGAGG AAGTCAAATT GTCTCTGTTT GCAGTTGACA
56651 TGATTGTATA TTTAGAAAAC CTCCTTGCTC CAGCCCCAAA TCTCCTTAAG
56701 CTGATAAGCA ACTTAAAGCA AAGTCTCAGG GTACAAAATC AATGTGCAAA
56751 AATCACTAGC ATTCCTATTA ACCAATAATA CACAAACAGA GAGCCAAATC
56801 ACGAGTGAAC TCCCATCCAC AATTGCTACA AAGAGAATAA AATACCTCGG
56851 AATACAACCT ACAAGGGATG TGAAGGACCT GTTCAAGGAG AACTACAAAC
56901 CACTCCTCAA GGAAATAAGA GAGGACACAA ACAAAATGGAA AAACATTTCA
56951 TGCTCATGGA TAGGAAGAAT CAATATCATA TCATAGGAAG AATCAGTGGC
57001 CATACTGCCC AAAGTAATTT ATAGATTCAA TGATATCCCC ATCAAGCTAA
57051 CATTGAATTT CTTACAGAA ATAGAAAAAA CTACCTTAAA TTTATATGA
57101 AACTAAAAAA GAGCCTGTAT AGCCAAGACA ATCCTAAGCA AAATGAACGA
57151 AGCTGGAGGC ATCAGGCTAC CTGACTTCAA ACATACTACA AGGCTACAGT
57201 AACCAAAACA GCATGGTACT GGTACCAAAC AGATATATAG ACCAATGGAA
57251 CAGAACAGAG GCCTCAGAAA TAACACCACA CGTCTACAAC CATCTGATCT
57301 TTGACAAAAA CAAGCAATGG GGAAAGGATT CCTTATTTAA TGTATGGTGT
57351 TGGGAAAACT GGCTAGCCAT ATGCAGAAAA CTGAAACTGG ACCCCTTCCT
57401 TACACCTTAT AAAAAAAAAA TTAAGTCAAG ATAGATTAAA GTCTTAAACA
57451 TAGACTTAAA CTATAAAATC CCTAGAAAAA AACCAGGGCA ATACCATTCA
57501 GGACACAGGC ATGGACAAAG ACTTCATGAC TGAATCACAA AAGCAATGGC
57551 AACAAAAGCC AAAATTGACA AATGGGATCT AATTAAACTA AAGATCTTCT
57601 GCACAGCAAA AGAACTATC ATCAGAGTGA ACCGGCAACC TACAGAATGG
57651 GAGAAAAATT TTGCAATCTA TCCATCTGAC AAAGGGCTAA TATCCAGAAT
57701 CTATAAGGAA CTTAAGCAAA TTTACAAGAA AAAAAACCC ACCAAAAAGT
57751 GGGTGACGGA TATGAACAGA CACTTCTCAT AAGAAGACAT TTATGCAGCC
57801 AACAAACGTG AGAAAAGGCT CATCATCCCT GGTTGTTAGA GAAATGCAAA
57851 TCAAAACCCC AATGGCATA CACTCTACGC CAGTTAGTTA AAAAGTCAGG
57901 AAACAACAGA TGCTGGCAAA TATGTGGAGA AATAGGAATG CTTTACACT
57951 GTTGGTGGGA GTGTAAATTA GTTCAAGCAT TGTGGAAGAC AGTGTGGCAA

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FIGURE 3T

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58001 TTCCTCAAGG ATCTAGAACC AGAAATACCG TTTGACCCAG CAATCCCATT
58051 GCTGGTTATA TACTCAAAGG ATTATAGATT TTTCTACTAT AAAGACACAT
58101 GCACACGTAT ATTTATTGCA GCACTGTTCA CAATAGCAAA GACTTGGAAC
58151 CAACCCAAAT GCCCATCAGT GATAGACTAG ATAAACAAAA TATGGCACAT
58201 ATACACCATG GAATACTATG CAGCCATAAA CAAGGATGAG TTCATGTCCT
58251 TTGTAGGGAC ATGGATGAAG CTGGAAGCCA TCATTCTCAG CAACCTAACA
58301 CAGGAACAGA AAACCAAACA CCACATGTTT TCACTCATAA GTTGGAGTTG
58351 AACAATGAGA ATACATGGAC ACAGGGAGGG GAACATCACA CACTGGGGCC
58401 TTTTTGGGGA TGAGGGGCTA GGGGAGGAAT AGCATTAGAA GAAATACCTA
58451 ATGTAGGTGA CAGGTTGATG GGTGCAGCAA ACCACCATGG CACGTGTATA
58501 CCTATGTAAC AAACCTGCAC GTTCTGCACA TGTATCCCAG AACTTAAAGT
58551 ACAATTTTTA AAAAGTAGGC AAAAAACAAA GAAAAGAAAA GTAATATACA
58601 ACCGAGACCT AATATTTTAG GCTTGCAACG ACAGATATTT TACTATTTAG
58651 TCTTTACAGG AAAAGTTTTT CAACTACTGC TTTATAGCAA AAATAATATT
58701 GTAGATGTGG AATTTATTGA TATAGCAGAG GGGTTTTTAG TAACTGATGA
58751 CTTAAGCAAG ATAAATACAA TTTTCACCGA TATGTGGTAT GCATGCTAAT
58801 ACAGCTTTTT TTAAGCATCT TAATATGATT GTTTATATTA CTCCACACAC
58851 CTCTCAAAAA AACTTAATAC CCTATTTTTT CTCTCATATC CTCCCATATC
58901 AGTTAATAGT ATCACCTTCC CAACTCCCCA CTGCCCCATC CTGTGTTCCA
58951 AGCTAGAAGT ATTGGGGTTA TCCTTTATAC TACCATTTCCT CTCACCTTCC
59001 AGATGCAGGT GGTCAACAGT CAGTTTTGTT AAGACATCAA TAGATTATCT
59051 TGCTTCCATT TCCTTGGTCA CTTCTTCATC CAGATCCTCC TTGCAGTAAA
59101 CGGGTCTCTC TGGCTTTGGT CTTAGCCCCC CAATAGAGGT AATACATGAA
59151 AGAGAATGTA TCAACAAATT GTACAGTCTT TTGAGTGACA ATATGTGCTA
59201 GGTATTTGTT CCATGTAAAA TTACTTCATT TGAATCCCAT GATGATAGAG
59251 TTAATATGAA CAATCATATT TTGTTTTTTT TTATATCCAG GTTATGAAAA
59301 CCAGGCTGGC TGTAGGCAAA ACTGGGCAGT ACTCTGGAAT ATATGATTGT
59351 GCCAAGAAGA TTTTGAAACA TGAAGGCTTG GGAGCTTTTT ACAAAGGCTA
59401 TGTTCCTCAAT TTATTAGGTA TCATACCTTA TGCAGGCATA GATCTTGCTG
59451 TGTATGAGGT GAGTTTGTAG AAATCTTTTG AATTGGAAAA TGCAGTTAGA
59501 TCTTGTTAGA ATTGGACTTT ATATGAAGAA GTAGATATAT ACCAGAAAAC
59551 AGTGTGTGAC CAGAAGTAAA TTCAAGCATG TGTATTTTGA ACTTTCAAGT
59601 AACTTGAGTG TGAATATGCA TGGGGTCACT TTTGTATTAG ATTTTCTTGG
59651 GAATTGCTTT TGTTAATGAA GAGTAGACTC AAAGTTAGGT ATAGTTGTTC
59701 ACCTTAAAAG GTGTTTCTAG AGATTTTTTC CTTTGTTTTG GATTTGCAAA
59751 AATCTGACAT TAAGCCAAGT GACTAATGTG ACTAACATGA GTAATACAGT
59801 TTCATTCCCT GTACGGAAGA ATACAAATCT TGGATCAACC CTGCAATCTA
59851 AATCATTTAA TAATTTATGA ATCTCAGAAA CAATTATTGA GCACACACTA
59901 TACAAACCAC TAGGTTAGAC ACTGGATCTG GGGATTCAAA GGACTCAATG
59951 TGTGCCTTGA AGAAACTGAA GGTCTGGTGG GGGAGACAAA CGACTAAAAC
60001 TCAGCTGGGT TATCTGTGCT GCGACAGACA TGAGCCAGGG TGCATGTTAG
60051 GATGAGACCT AAGCTACAGC GTAGAGGAAG AGTGGAATGT GTAATGAAAA
60101 GAAGAGTCGA ATTTTTTTTT TAAAGAGCTT TATTGAGATT TAGTTCATAT
60151 TCCTTACATT TCACTCATTT GAAGTGACA AGCAAATGGT TTTTGGCTTC
60201 TTACATAATT TTTAAAAATT ATTATAAAAT ATAAAATTTG CCATTTTACT
60251 AATTTTAAAG GTACAATTCA GTGGCATTAA TTACATTAC AATATTGTGC
60301 AACCATCAAC ACTATTTCCA AATCCTTTTC CTCCTCCAA ACAGAAACAC
60351 CTTAACCTTT AAGCAATAAC TTCCTACCT CCGTAACTCA AACCTTTGGT
60401 AACCTCTAAT CTGCTTTCTA TGCTAGGAA TTTACCCATT CAAGATATCT
60451 TATAAGTAGA ATCATACAGT ATTTTCTTT TTGTGCTGA TTTATTACTC
60501 TTAGCATAAT GTCTCTAAGG TTTGTTTCATG TTGTAGCATG TATCAGAACT
60551 TCATTTCTTT TCATGGCTGA GTAATATTCC GTTATGTGTA TATACCACAT
60601 TTTGTTTAGT CCTTCATCTG TTGAAGAGCA TTTGGATTAT TTCTACTTTT
60651 CCAACATTGT GAATAATGCT GCAGTGAACA TTGGCATCTG CGTATCTGTT
60701 CGAGTCTATG CCTTCAATTC CTTTGGGTAT ATATCTCAGA ATGGAATTGC
60751 TGAGCCATAT GGTCAATCTG TGTTTAGCTT TTAGGAACTA TGAGACTGTT
60801 TTCCATAGTG GCTGCACTTA CATTCTCACC AGCAACATAC AAAGGTTCCA
60851 GTTTTTCCAC GTCCTTATTA ACACTTAATT TCCATTTTAA AAAAGCTTAT

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FIGURE 3U

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60901 TTTTATTATG GCCGTCCTCT TAGGTGTGAG GTGGTATGGT TCAGGACTTT
60951 ACTTCTTGTG CTGAGTTTTT TAAAAAATTG TGATTAACAA CACATAACAT
61001 AAAGTTTATG ATTTTAACCA TTTTAAATA TATAGTACAG TAAGTGTTAA
61051 CTGTTTGTGG TTTGTTGTGC AACAGATCTC TAGAACTTTT TCACTTCTCA
61101 AAACCTAAAC TCTATAGTCA TTAAACAACA GCTCCCAATT TCCCCTTCAC
61151 CCCAGCGCTG TGTAACCTAC TTTCTCGTTT TATGAGTTTG ACTACATTAA
61201 ATACCTTGTA TAAGTGAAAT CATGTGGTAT TTCTCTTCC GTGACTGGCT
61251 TATTTTCATG AACATAGTTT CCTCATGATT CATCCATATG ATAGCATACA
61301 ACAGGACTTT TTTGTTTTTA AGGCTGAATA ATAATTTGTT GGGTATATAT
61351 ATCACAATTT CTTTATTCAT CTGTTGATGG ACATTTGGAT TGTTTCTACA
61401 TCTTGACTAT TGTGAATAGT GCTGCAGTGA ACATGGTTGT GCAAATATCT
61451 CTTCAAGATA CTGTTTTTCTG TTTCTTTTGA CATATACTCA GAAGTGGAAT
61501 TTCTGGGTCA AATGGTAATT CTATTTTTTA GTTTTTGAGG AACCTCCATG
61551 TCATTTTCCA TAGTAAGTAG ACCTTTTTGT TTTTAAACAT TTCTATCAAT
61601 GTACACCAAG ATTCCAATTT CTCCATGTCC TCCCAACAC CATTAAGTGG
61651 GGTGGTGGTC TACTACTATT GCTGTGTTGC TGTTTATCC TCCCTTCAGT
61701 TCTGTAAGTG TTTGCTTCAT ATATTTAGGA GCTTAATATT AGGTCCATAT
61751 GAAGTTATAA TTTCTTCTG GTAAAGTGAC CAATTTATCA TTATGTAATG
61801 TCCATCTTTG TCTCTTGTA CAGTTTGTGT CTTAAATCT ATTTTGTCTG
61851 ATGTAATTAT GGCCACCCCT TTTCTCTTTG GGTCCCGTT TTATGGAAT
61901 ATCTTTTCC ATCTTTTCC TTTTCTTTA TGTGTGCTCT TAGATCTAAA
61951 GTGAGTCTCA TAGATAAGGT ATAGTTGATT CTGTATGTTG TATTTACTCA
62001 GCAATTTATA TCTTTTAGTT AGGGGATTTA ATCCATTTAC ATTTAAAGCA
62051 GTTACTGATA GGGGAAGGACT TACTGTTGTC ATTTGGCTAG CTACCTTTTT
62101 ATCTTTGTCC TGTGGCTTTT CTGTTTTTCC CTCTCTCTCT TCCTGGCTTC
62151 TTCTGTGTTT TGTGATTTT TTTTTTTTT GTAGTGATAT GTTCTGATTC
62201 CCTTCTCATT TCCCTTTGTG TGCATTCTAT AGATGCTATT TTTGTGGTTA
62251 CCATTGCAAC TACATAAAGC AACTAAAGT TATAGCAACT TATTTAAGC
62301 TGTTTACAAC TTAACCTCAG TGGTATATAA AACTCTATTT CTTTACATAT
62351 TTTACCTCCT CCCCACAAAC TTTATGCTCT TTGATATTGT ATATCCTTAA
62401 CATAGATTTA TAGTTACTTT TTATGCTTTT CTCTTTTAAA TTCTGTTTAA
62451 ATTTTGTTTT TGAAATTTAG ATTTTCAAGT TATTTATATA CCTTCATTAC
62501 AATACTATAG GATTTTATAA TATTCTAAAT ATTGACCTTT ACCATAGAGT
62551 TTCATATTTT GTGGTTTGT GTTGCTATTT ATCATCCTTT TGTTTCTCCT
62601 TTTAGCCTTT CTGTAGGGC CGGTCTAGTG GTGATAAGCT GTATCAGCTT
62651 TTGTTTGTC GGGACAGTCT TAATTTCTCC TTTTGAAG GGCAGTTTGT
62701 CCCATACAGT ATTTTGTGTT GGCAGTTTTT TTAAGTTTCA AAACATAGAA
62751 TATAACATTC CATTTCTTTC TAACCTGCAA GATTTCCATT GAGAAATGCA
62801 CTCAATGGAT TTTTAAATCC ATTGAGATAA TTTTAAATC CTGTAGGATT
62851 TAAAAATTTT AGTCTTACAG GATTAACAAA TTAAGAGTTT AAACCTTGTA
62901 TATAACATAT TAACATGTAT TTTATACTTA AAGTATCTTA TGTTTAAAAA
62951 GTTGATTATC ATATATATTT TATACAGTTT CTCCTAATTA TTGCCTTCTA
63001 ATGAAATACA GGGACCTAGA GTAACAGGGA TAAAGTATGG CCTTTTGATC
63051 AGCACGCCTG GTTCTGAGTC CTTCTTAAAA AAACCTCTGGG CCTGGTGTGG
63101 TGGCTCATGC CTATAATCTC AGCACTTTGG GAGGCCGAGG CGGGCGGATC
63151 ACCTGAGGTC AGGAGTTTGA GATCAGCCTT GCCAGCATGG TGAAACCCTG
63201 TCTCTACTAA CAGTACAAAG ATTAGCTGGG CGTGGTGGTG GGTGCCTGTA
63251 ATCCAAGCTA CTCAGGAGGC TGAGGCAGAA GAATCGTTTG AACCTGGGAG
63301 GCAGAGATTG GGCCACTGCA CTACAGCCTG GGTGACAAGA GCGAGACTCC
63351 ATCTCAAAAA AACAAACAAA AACTCCGCTG AGATGAATTT TTCTCATTTT
63401 TAAATCAGA ATAATAGATT TATGTAAGAG TTTCTGTAAG GCTCAAATGA
63451 AATATATGTA ACGTGTAAAA TGAGATACAA TTAGTAGAAT TATATTATTT
63501 TATTAATACT CACCAATAAG GGTGTTCTTT AGATCCTGCA GCGTTTGCTG
63551 CGCAGTTTAC GTTTGTTTAG AAGAATGTCA GTAACCGGTG CAAACCTCAT
63601 GTGTTCCGCA CCCCCAGTGG CCTCCACCT CTCCACAGAG TCACCGCCTC
63651 CTGCAGTGCC TGCTGCTTCT GCAAATGCGT GGCCTCATCC TGCAGAAACG
63701 GGGCTTCTCA TGAGGTTGAG AATAGCTGTG AAAATGTTTA CGTTGAAGTT
63751 GTAGAGTTG TTAATTATTT TCTTCTTTAT TTCTCTGGCA GCTCTTGAAG

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FIGURE 3V

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63801 TCCTATTGGC TGGATAATTT TGCAAAAGAT TCTGTAAACC CTGGAGTCAT
63851 GGTGTTGCTG GGATGCGGTG CCTTATCCAG CACCTGTGGT CAGCTGGCCA
63901 GCTACCCATT GGCTTTGGTG AGAACTCGCA TGCAGGCTCA AGGTGAATTT
63951 TTGATTACAG AACCACACCG ATAAAAGTGC TGCACCAGTA ATGTGCTTTT
64001 AGAACTCCAA GTTCTACTAA GATGCAGACT GTAGTTTAA GACAGTATTT
64051 CTCAACCTTT TTTTCATTAT TGCCTCCTTA AGGAATCTTT TCAGAAATTC
64101 TTTTTCTAAA TGCTCCCTCG TCATGAAATT TTAATGCGAC AGAAGCATTG
64151 CATATGTA CTATGCATAC ATATGCCTTA TAGATAAACA GAGTACTATT
64201 TTTTTTGACT GTGTTACATG CACGTTTTAA GATTATAAGC TTTAGTATCT
64251 GATGGATTTG GGTTCAGATC CTTGCCTCAG ACTTCTTGGG GTTTTTAATG
64301 GGAATGAAAA TTGTACAGTG TTGTAAGAAT TACCAACAAT ATAAATAAAG
64351 CATCTTGGGT TTGTTAAATT TTTGGTAAAT GGTGGTTGGA ATCATTTTTT
64401 AGTGTTGCGT AGACCCTACA AGTTTTGAGC TGTGATTCCT CCTCACTGTG
64451 ACACTGTCTC CATTGTTGGC TTTGATTACA CTGTACCATC CTGGTTGTTT
64501 TGCCAGCCCA TTGATAACTT TTACCATTG CTGGCTTTTA TTGCTATCCC
64551 CACTCTATTA AAGTATGCAT TCAAATGCCT TTCTTTTCTC TTTGATGCTT
64601 TCCCTGGTCA GTCTTATCCA TTGTTTTCTT AAGTAGTACA CCTTGGGCAT
64651 CTACAGTCTT ATTCCCAACC TCCCTTCCAA GTGCCAGCCA CAGCAACCCC
64701 AGCCAAAGCAG TCAGTAACATA ATTGGCAAAT ACTCCCTGAG CCATTGTCCC
64751 ATTCTAGACA CTGCCAGATG CTAGGGGTAG AGCAGTCAAC AAGTCAGGTG
64801 TGGCCCCGCC AGTGTAGAGT AGAGAAGACG TTATGTCCAG CAAGTAAACA
64851 ACCTGGTTAA ACCAACTCCT CTTTTGTTAG GGGAGCACAG AGCAAGGAGC
64901 TATAACCTAA CTTGGGCGCT GCAGAAATGCT GTCAGTGAAG CTGAGACTGG
64951 AAAGATGAGT GGGAGTTAGC TGGGCACAGG CCAGTGGAGT GGGAACAGAA
65001 AACATTCCAG TTGAGGGAAA GCATGTGTGA AGACACTGAG GCAGGCACCA
65051 ACATGGTGTA TTTAAGGAGC TGAGAGACAG TCATGGCTGT AGAGAAAAAC
65101 ACAAAGTAGT GAACTACACG TTTCTTGTGT ATTCTCTCAT TTCACCATCA
65151 TAACCATCTT GGGGATGGGA ATACTAACAT TATCCCCATT TTTCAGATGA
65201 GCAACTGGGG CAGAGAGAAT TTAAGTAACT CCCACAAGAT TATACCTGTG
65251 GTAAAGTAGT GGACTGAAAT TCAGACACAT GCAGTCTGAT TCTAACCCCTC
65301 CTGTCTGCCA GCTCTGATCC AGAACTTTGC ATGACTGATA CGGCTGATAG
65351 ATTGTCTATG GCTGATAGAC TGTCAATTTCT GACCTAAAAG TCTGATCATT
65401 TTACATCTGT TCAGACATCT TTGCAGCCTT TCGGTGTCAG TTCCAAAGTT
65451 GTTAGTGGGA ATTTCAAAGC CTTTAATAAT CTAGCCCCAC TTTGTTCACT
65501 CTCTGTGTAA TAACCACATA CAACAATTGG CTGCATCTCC ATAGCACATG
65551 GTA CTCTCC CGTTGTCTTG GTTGTGCCAG CAACACTGGT TTTGCTTTTC
65601 TCTTCTCTGT TGTGAGGTC ATTTCCAAGG CCCAGGTCTT TGTGCTTTTT
65651 CCAAGCTTC CCAGAGCTTC TTCCATACTC CCCTTACTTC CTGAGATTTA
65701 ACTGTTCTCT CTTCAGCGCT TGTCTAGTAA GAAGGAGGCA GCAGCAGCAC
65751 TGTGGGGTGG TGGAAAGTGT ACCAGCTTTG GAGTCAGACC ATTGGATCTC
65801 AGCCCTACCA TTTTCTACTT AGATTTTTTT AGGACAAATT TCTCCATCTT
65851 TCTAAGCCTC CAATTGCTCA CTTACAAAAT TGATATAACA TTTACCTTGC
65901 AAGATTGGTA TGGAAGGTAA TTAACCCAGT ATTTAGAACA TAGTAATTAA
65951 TAAATAACTA TTATTACCAT CATTACTATA GTTAGGACAC TCACTGTTAG
66001 GTGCTATACA AAGAGGATCA TAAAAGGGAT GTTGTCTTGG GCTTCTTGGA
66051 ATAAATGTTG TCCTTTTACT GTATTTTAGA ATATCATTTCT GGGTCATAAT
66101 TGTTTGTGTG CATAATAATG AAACATACTT GAATATTTAA TTACCCTCTT
66151 TTTTTATTTT TTAGCCATGT TAGAAGGTTT CCCACAGCTG AATATGGTTG
66201 GCCTCTTTCT ACGAATTATT TCCAAAGAAG GAATACCAGG ACTTTACAGA
66251 GGCATCACCC CAAACTTCAT GAAGGTGCTC CCTGCTGTAG GCATCAGTTA
66301 TGTGGTTTAT GAAAATATGA AGCAAACCTT AGGAGTAACC CAGAAATGAT
66351 GTTGCAATTT TTGCTTTAGC CTGATAATTG AAACCTTCAA CAATCTCTGG
66401 AGTGACTTTT TCTCCTCGAA TTGAAACAAG TCTATGGCAA AAGAAGCTGC
66451 ATTTTTTTCA CAAAAGGGAA GATGGTAACA ATGGTCACTT CAAACTTTTG
66501 GGCTAAATTA TATGTACACA GAAATGTTCA AAATCATAGT TTTAATGTGT
66551 TTTGAAAAGG CCACACAATT ATACTTTATC TTTTCTTAAT AATCCTGCAA
66601 ATCTCTGCCC TGAATCCGAA ATCTGAAAAT GTACTGGCTT GAACAAAATT
66651 TGTTTTGTGT GTTAGAGTTA TAAATCATTA ATCTTTATTT CGGGTGGTTT

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FIGURE 3W

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66701 ACGTTTATGC CAGTTCCTTT ATATTTAAAT TTCTTGTTTT ATATATTTTG
66751 AATGCTTTTA TAGATTTCTT TAAATTTCTT TATAGAACCA TTAATAGAAA
66801 ATCATTACAT TTTAAATATA CCTTACAGCA AAAGCATCCA AATAAGTATA
66851 GGGTTTATGT CCTTATTTTT CTTCAGCTG AATACGAATG AGCACAGTGG
66901 TGGAAATTTCT GAAGGGAAGT GATGAAATTA TATTTATTTT AGTGGGCACT
66951 TTTCCATTTT ACCACTGTAC CATTATTTGG TTCCTGGAGT TATACACTAA
67001 TTTTCAGTAT ATTACTGTTA AATTACCAAC ACAAGGCAAT TTATTTGAAA
67051 GATTCCGTTT ATCCTGCCAT TGCTTTGAAA AGCAGCAGGA AACGAAATCC
67101 TTTGACTTGT ATCAGCTTCT GCAGAGCATC TTTGTTTTCC TTTGTCCTTT
67151 GTTTCCTACC TTTTGAATCA GATTCCGTTT TAGTCAGGAA GACTTCTTGG
67201 GACCATTCTT AGTAACCTGA AATTTCTTTT TTAATTGCAT GAAGTGGATT
67251 GATCATGAGC AAATGATGTG CTTATTTCTC CCTCACTGTT GAATATCTTT
67301 GAACTTGCTG TTTTCAATAT GGCAGCACA AAGGTGAGAG ATACATATTA
67351 ATAGTAGTAT GTATTACTCT TATACATTAG ATACCTATAT TTAAATGAAA
67401 GGCCCAATTT GTAAACATAT ACATTCATAT TCTCTCTTGC CCCAAGTTTT
67451 AGGAACATGT TAGGATATAG GAGACTTAAT TTATAATAAT GAGAGCATTT
67501 TTTTATTTTA CTAAAGCCAT TTTTATAGTC AACTATCTTT TCTTATTTGT
67551 GTGATTAGAA CTTGAAAAA TATTACTAG TTGAAGTTAT TATCAGTTTT
67601 TAATTTAGTT CTTAAACTCA TTTCACTTCT AATAATTTCT GTTATAAATT
67651 GCCAGCATTT TAATGAAAAT CTAATGATGT AATAGGCATT TTCTTTATTT
67701 GAACCTACCT CTTTATTTTT CTGAACCAAA GAGAAAGATG GACTGGTGTG
67751 TGTGAAACAT TTTTAAAAAT GTAGTTTCAT TTATATTAGT TATGTTTGAT
67801 AAATGTCTCA GTATTTTTAT AATATGATAA GCCTGGGATT CTACTTTTAG
67851 GGTATTTTGT ACTTTTGAGT AATATATAAA GTGACAATAT TAAGGTACAT
67901 GATCAGCTCT TTCTATTTTT ACTCGTAAAA ATTATGGAAT TGAATAAATT
67951 TGCTAACAACT TTTGAAATTT CAAACTTCTG GAAAATATGA AAATATTCAT
68001 TGTTCAATAT GAATTTAAAT TGTAAGGTAT GAATGTGATT TGTCTGTACA
68051 TCTTGTATCT TTTCCAAAAA ATGATTCTGT ATCTTTTGGA AAAAAGCCGA
68101 GAGTTGAAGA TAGTATATTT CTGGTAGTAC TGAATATTTA CTTACAGTTT
68151 CTATCAAAAA TATATATTTG TTTCTAAAAA TACTTGTTTT CCAGTTTTTA
68201 TTTTTTTTGT AGAAAAATTCT TAAGTCTCAG TTTCTTAATT GAAAAAATAA
68251 AATTATAAAT AAAGCAAAAA TTGTATCTTA CAGCTTAGCT AGCTTAGATG
68301 TTTGGCACCA GTTTGAATCA TGCTTTTTAC AGCTGGCTCC ATGTAGTCTT
68351 TCCAAACATT TTGGCCTTTC CTGAGCAGCC CTTGTAGATA TTGTCTGTAT
68401 GATGCATTTT GACACAAGGT GATATTTTTT GTGATATCAA AATTCCACAT
68451 TTACCCATTA GAGTTACAGC CCTGGGGTTC ACAGTACCAA GGGGGACCCA
68501 GAGCCTCAGG ATTGGCCAGG CTCATTTTGC CGTGGAGTAT CAGTTTGTCT
68551 TGAAATTGTG GGAAAAAATT CTAAGTTGAA TTCACTGGTA AGTAATTTTT
68601 TAAATTTTCA TAATGCAGAT TACATCCAAA ATTTGATTTA AAAATTAATA
68651 CATAAGACTG CAGAGAAATT CTGCATTTCA ACTCCAATAC TATCCAGACT
68701 TCAGAAATAA GTTATCAGTT ATTTCTGTAA GCTTCTTGCT TACCTGGATA
68751 CCTGACAGGT GAGATGGCTG TAGCAGACAC TGGCAGTTCC CTGCCACAC
68801 ACCTGTCCCT GTCCACAGCT GCACAAGGCA GCTCTGTGTG CAATTGCCAG
68851 CATCTGCTCC TCTGTTCTCA GGAATCTTTT GTTAGAAAAA TGCTGCCATA
68901 TTTGTTTCTC ACCTATTAGT CTTGTCTCCC AGTCAAGAGA ATAAATTTAT
68951 GCAAGCAGAG ATTGTACTTT ACAGTATTTT GTCTTTGAGC TTGGCATTAG
69001 GTTGCAATTTG TAAAAATGTG GCATGGCTTC CTCATCCCCC AATAGGAACT
69051 TTGCCAGCCC TTTTGTCTC ATGGAACCTC CTTTTTTGAA AAGAGCACCA
69101 AAGGAGTAAA AATACTGTGG AGGGAGCAAC CCTCCTTTGC CATATGCTCT
69151 CATTGGGAGA CATGTGGAGC AGTCTGAAGT CATTTAGGCC ACTCTCTGGG
69201 AGAGCACATC CTATGATGTT CTCCCAGCCT AGCCCCTTCC ACTGTGCTCA
69251 AGTCCAAGCT GACCAGCTTT CTGACCACAG TGTAACAAA GATGATTGTC
69301 AGTGGGCCCC AGAATCCTAT ACCCAGA (SEQ ID NO:3)

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FEATURES:
Start: 2132
Exon: 2132-2314
Intron: 2315-17055

FIGURE 3X

Exon: 17056-17182
Intron: 17183-20983
Exon: 20984-21071
Intron: 21072-41719
Exon: 41720-41831
Intron: 41832-45391
Exon: 45392-45550
Intron: 45551-47878
Exon: 47879-48031
Intron: 48032-54612
Exon: 54613-54720
Intron: 54721-59290
Exon: 59291-59458
Intron: 59459-63791
Exon: 63792-63942
Intron: 63943-66164
Exon: 66165-66346
Stop: 66347

CHROMOSOME MAP POSITION:
Chromosome 1

ALLELIC VARIANTS (SNPs):

DNA				
Position	Major	Minor	Domain	
1722	G	C A	Beyond	ORF(5')
1767	C	G A	Beyond	ORF(5')
1840	C	G	Beyond	ORF(5')
1857	T	G	Beyond	ORF(5')
1945	G	T	Beyond	ORF(5')
2007	A	C	Beyond	ORF(5')
2769	C	G	Intron	
3664	C	T	Intron	
3827	G	A	Intron	
4113	C	T	Intron	
4337	A	G	Intron	
4473	G	A	Intron	
6455	T	G	Intron	
6533	T	G A	Intron	
6919	G	C	Intron	
7305	G	A	Intron	
7340	A	G	Intron	
7466	A	G	Intron	
7589	G	C	Intron	
7810	A	C	Intron	
9104	G	A	Intron	
9503	A	T	Intron	
9898	G	C	Intron	
10196	T	C	Intron	
12327	C	G A	Intron	
13749	G	A	Intron	
14150	T	C	Intron	
14529	G	A	Intron	
14653	G	A	Intron	
15871	A	G	Intron	
19244	G	A	Intron	
19387	T	G	Intron	

FIGURE 3Y

19447	C	G	Intron
20076	T	C	Intron
20492	T	-	Intron
20868	T	C	Intron
20941	T	C	Intron
21116	C	T	Intron
21701	G	A	Intron
21710	A	-	Intron
21826	C	T	Intron
21840	-	T	Intron
21841	-	C T	Intron
21843	-	C	Intron
22045	C	A T	Intron
22061	G	T	Intron
22348	-	A G	Intron
22682	A	G T	Intron
22783	-	T	Intron
23448	A	G	Intron
24960	G	A	Intron
24983	T	C	Intron
25390	T	C	Intron
26060	C	T	Intron
30245	C	G	Intron
33664	G	T	Intron
33883	C	A	Intron
34373	G	A	Intron
34558	G	T	Intron
43929	T	A	Intron
44309	T	- C	Intron
44997	T	G	Intron
46538	A	G	Intron
48153	T	C	Intron
48288	G	T	Intron
48412	G	A	Intron
48446	C	G	Intron
48456	G	C	Intron
48789	C	-	Intron
48859	G	C	Intron
49126	A	G	Intron
49378	T	G	Intron
49482	A	C	Intron
49741	G	A	Intron
49840	A	G	Intron
50102	G	A	Intron
50109	C	G T	Intron
50747	G	A	Intron
51272	G	A	Intron
52842	G	A	Intron
61837	A	G	Intron
62018	A	G	Intron
65562	A	G	Intron
65780	G	A	Intron
66092	G	A	Intron
66617	C	T	Beyond ORF(3')
66892	G	A	Beyond ORF(3')
67263	G	A	Beyond ORF(3')
67651	G	T	Beyond ORF(3')
67935	C	T	Beyond ORF(3')

FIGURE 3Z

69000 T G Beyond ORF(3')
69134 C T Beyond ORF(3')

Context:

DNA
Position
1722

TTGCCACGCAGATGGCTGTTGATCTTTCTGCAACAAATCCAGGAGTTTCTCCTTTTGT
TTTTATAATTGCTCCAATAGATGCTTTAGGATTTAACTCTCTGCTTTTAAAGCAGAATC
GCCATCCCAGGTGTGCAACCACGAAAAAATTAGACATCCGTGAGAGACAATGCCCTCCAT
GGCCAGTTTCCAGGCAGAGAGAAGCAGCTCTGGGCTGACCGCCAAGGCTCCGGCCCGAG
AGGGTCTTTAAGTGGAGTAACCACTCTTCAAGACCCCGTCCCAAGCCACCGACGCGCTG
[G,C,A]
CGCTGCAGCCCTGGACCTGCTGGGGGCTCTTCTCGGACCCGCATGCTGACAGCGGGAC
TGGCAACTGGGCAGAGGTCGACCCCGGTCCGCACAGCACCTCCCGAGACCCAGTCCCA
GCTCCCTCACTTCCGGCTCTCTGGAGGCGGGCCCGCCAGTGCCGCGGAGGCCAGCGCGG
CGAGCTCCTCCCGAGCAGCGGCGGACGGCCACACCTGCGCGCCCGCGGGCTCGGGTG
GGTCTCCGCTCCTGCGCCCTGCGCGCCGACCGCACCCCGACGGCGCCCAACGCT (SEQ ID NO: 35)

1767

AGTTTCTCCTTTTGTGTTTATAATTGCTCCAATAGATGCTTTAGGATTTAACTCTCTGCT
TTTTAAAGCAGAATCGCCATCCCAGGTGTGCAACCACGAAAAAATTAGACATCCGTGAGA
GACAATGCCCTCCATGGCCAGTTTCCAGGCAGAGAGAAGCAGCTCTGGGCTGACCGCA
AGGCTCCGGCCCGAGAGGGTCTTTAAGTGGAGTAACCACTCTTCAAGACCCCGTCCCAA
GCCACCGACGCGCTGACGCTGCAGCCCTGGACCTGCTGGGGGCTCTTCTCGGACCCGC
[C,G,A]
TGCTGACAGCGGGACTGGCAACTGGGCAGAGGTCGACCCCGGTCCGCACAGCACCTCCC
GAGACCCAGTCCCAGTCCCTCACTTCCGGCTCTCTGGAGGCGGGCCCGCCAGTGCCG
CCGAGGCCAGCGCGGAGTCTCTCCCGAGCAGCGGCGGACGGCCACACCTGCGCGCC
GCGCGGGCTCGGGTGGGTCTCCGCTCCTGCGCCCTGCGCGCCGACGCGCACCCCGAC
GGCGCCCCAAACGCTGTTGCGCGCGCGCCCGCCAGCCCGGCTCGCGCTGGTCCCGG (SEQ ID NO: 36)

1840

TCGCCATCCCAGGTGTGCAACCACGAAAAAATTAGACATCCGTGAGAGACAATGCCCTCC
ATGGCCAGTTTCCAGGCAGAGAGAAGCAGCTCTGGGCTGACCGCCAAGGCTCCGGCCCG
AGAGGGTCTTTAAGTGGAGTAACCACTCTTCAAGACCCCGTCCCAAGCCACCGACGCG
TGACGCTGCAGCCCTGGACCTGCTGGGGGCTCTTCTCGGACCCGCATGCTGACAGCGG
GACTGGCAACTGGGCAGAGGTCGACCCCGGTCCGCACAGCACCTCCCGAGACCCAGTCT
[C,G]
CAGTCCCTCACTTCCGGCTCTCTGGAGGCGGGCCCGCCAGTGCCGCGGAGGCCAGCGC
GGCGAGTCTCTCCCGAGCAGCGGCGGACGGCCACACCTGCGCGCCGCGGGCTCGGG
TGGGTCTCCGCTCCTGCGCCCTGCGCGCCGAGCCGACCCCGAGCGGCGCCCAACG
CTGTTGCGCGCGCGCCCGCCAGCCCGCTCGCGCTGGTCCCGGTCTCGCCCCGACG
CCCTCGATCTCCCGTGAATCTCTCGGCCAGGCGCCTGCGCCTCTGGGACCATGTTGCGC (SEQ ID NO: 37)

1857

CAACCACGAAAAAATTAGACATCCGTGAGAGACAATGCCCTCCATGGCCAGTTTCCAGG
CAGAGAGAAGCAGCTCTGGGCTGACCGCCAAGGCTCCGGCCCGAGAGGGTCTTTAAGTGG
AGTAACCACTCTTCAAGACCCCGTCCCAAGCCACCGACGCGCTGACGCTGCAGCCCTGG
ACCTGCTGGGGGCTCTTCTCGGACCCGCATGCTGACAGCGGGACTGGCAACTGGGACG
AGTTCGACCCCGGTCCGCACAGCACCTCCCGAGACCCAGTCCCAGTCCCTCACTTCC
[T,G]
GCTCTCTGGAGGCGGGCCCGCCAGTGCCGCGGAGGCCAGCGGGCGAGTCTCTCCCGAG
CAGCGGCGGGACGGCCACACCTGCGCGCCGCGGGCTCGGGTGGGTCTCCGCTCCTG
CGCCCTGCGCGCCGAGCGCACCCCGAGCGGCGCCCAACGCTGTTGCGCGCGCGGCC
CCGCCCGGCTCGCGCTGGTCCCGGTCTCGCCCCGAGCCCTCGATCTCCCGTGA
CTTCTCGGCCAGGCGCCTGCGCCTCTGGGACCATGTTGCGCTGGCTGCGGGACTTCGT (SEQ ID NO: 38)

1945

CAAGGCTCCGGCCCGAGAGGGTCTTTAAGTGGAGTAACCACTCTTCAAGACCCCGTCCC
AAGCCACCGACGCGCTGACGCTGCAGCCCTGGACCTGCTGGGGGCTCTTCTCGGACCC

FIGURE 3AA

GCATGCTGACAGCGGGACTGGCAACTGGGCAGAGGTCGACCCCGGGTCCGCACAGCACCT
CCCGAGACCCAGCTCCCAGCTCCCTCACTTCCGGCTCTCTGGAGGCGGGCCCGCCAGTG
CCGCCGAGGCCAGCGCGCGAGCTCTCCCCAGCAGCGCGGGACGGCCACACCTGCGC
[G,T]
CCGCGCGGGCTCGGGTGGGGTCTCCGCTCCTGCGCCCTGCGCGCCGAGCCGACCCCGG
ACGGCGCCCCAAACGCTGTTGCGCCGCGCGCCCCGCCCAGCCCGGCTCGCGCTGGTCCC
GGTCTCGCCCCGAGCCCTCGATCTCCCGTGACTTCTCGGCCAGGCCGCTGCGCTCT
GGGACCATGTTGCGCTGGCTGCGGACTTCTGTCTGCCACCGCGGCTGCCAGGACGCG
GAGCAGCCGACGCGCTACGAGACCTCTTCAGGCACTGGACCGCAATGGGGACGGAGTG (SEQ ID NO:39)

2007 GCCACCGACGCGCTGACGCTGCAGCCCTGGACCTGCTGGGGCCTCTTCTCGGACCCGC
ATGCTGACAGCGGGACTGGCAACTGGGCAGAGGTCGACCCCGGGTCCGCACAGCACCTCC
CGAGACCCAGCTCCCAGCTCCCTCACTTCCGGCTCTCTGGAGGCGGGCCCGCCAGTGCC
GCCGAGGCCAGCGCGCGAGCTCTCCCCAGCAGCGCGGGACGGCCACACCTGCGCGC
CGCGCGGGCTCGGGTGGGGTCTCCGCTCCTGCGCCCTGCGCGCCGAGCCGACCCCGA
[A,C]
GGCGCCCCAAACGCTGTTGCGCCGCGCGCCCCGCCCAGCCCGGCTCGCGCTGGTCCCGG
TCTCGCCCCGAGCCCTCGATCTCCGTGACTTCTCGGCCAGGCCGCTGCGCTCTGG
GACCATGTTGCGCTGGCTGCGGACTTCTGTCTGCCACCGCGGCTGCCAGGACGCGGA
GCAGCCGACGCGCTACGAGACCTCTTCAGGCACTGGACCGCAATGGGGACGGAGTGGT
GGACATCGCGAGCTGCAGGAGGGGCTCAGGAACCTGGGCATCCCTCTGGGCCAGGACGC (SEQ ID NO:40)

2769 TGGGGCCGCGACCGGCGACCCCGGTAACAGAAGTGGGTCTAATACGAAAGTCTACTGGT
ATTTGTCCAGATAAAATGAGTGTGTGGACACTCTGGCCACGGGCACTGTTAAATTTT
AAGACACTTTTGTCTGAATCCATCCAGGTTCTTTGTTTTCTGTTTTAATACCTTGAG
ACATGTAATCCGTTTTAGCTGTCAGACTTCAGTGGGTCCCAAGTTTTGTATAAAGCGCA
CACATTGATCTCTTTCGAAGCTGCTTTGTTACAGCAGCTATGTGTATTGTCTACTGTTT
[C,G]
AAAAGTGTTTGAAAACCAATCGCGTGTTCCTTCTGTTGAGAAGGAATGGCGGC
ATTCCATTGTTTAAGACATTCTAGGTTAATGCCCTAGGTACATAAATTGATCTGAAGGG
TTGACTTGCACTGCGACTGAGCAATTTTCTTCTGAGTCATCTTAAGTGTGCCCTG
AACTTCTGCCCCCTTAGTAGGGTGGAGATATGTGAACTTCTCAACCCTGTTGAAGCGT
TCCCTGACACTGGCATTCTCTTATCAAAGAGGGAAAGTGATTAGGTTACTATGAGGGCC (SEQ ID NO:41)

3664 GCTGATTGTCCAGAAATGGCCAGTTGGAGTTCACCACCATGTCCAATCATTGGCTGGA
AGCAGCCAGGAAAGGGACGACCTTGCTGCAGTGCATCAGCAGATGCCAGGGTTAGAGGC
TAGAGAGTGGAAAGTCAACTGTGTTCTCACAGTAGGTGCCCTTTGAAGGGAGATCTCAGTG
GTACAACTCCATGGTCCCTACAATATACAAAAGCTCTTTGGAGTGCTCAATGATTTTTAA
GATTGTAAAGGGATCCTGAGATCAAAAAGCTTGAGAAATTGCTGCTGTATCACCATTTTTA
[C,T]
GTAAGTGCATCATATTCTGTTATATGTTTGTGTCATAGTATATGTTACCAATTCTTTTA
AATCACCTTTTACTTTATTGATAGTTTAAAAACGATTGTAAGTGAAATTGCAATGGATGT
CCTTTGTATTCATTTTCTATTCTGGTCCAGTTACTTTCGTAGGATAAATTTTGAGGAGT
GGACATTGCTGAGTCTGAAGGTAACACACATTTTAACTGGGATACGTATTGCCTTTCCG
AAACCTTAGACCCATTTTCACTCTTTGACTGACAGTGCTTGCTTCTCCACATCCTCGCT (SEQ ID NO:42)

3827 GAAGGGAGATCTCAGTGGTACAACCTCATGGTCCCTACAATATACAAAAGCTCTTTGGAG
TGCTCAATGATTTTTAAGATTGTAAGGGATCCTGAGATCAAAAAGCTTGAGAAATTGCTG
CTGTATCACCATTTTACGTAAGTGCATCATATTCTGTTATATGTTTGTGTCATAGTATA
TGTTACCAATTCTTTTAAATCACCTTTTACTTTATTGATAGTTTAAAAACGATTGTAAG
TGAAATTGCAATGGATGTCCTTTGATTCATTTTCTCATTCTGGTCCAGTTACTTTGTA
[G,A]
GATAAATTTTGAGGAGTGGACATTGCTGAGTCTGAAGGTAACACACATTTTAACTGGGA
TACGATTGCTTTTCGAAACCTTAGACCCATTTTCACTCTTTTACTGACAGTGCTTTC
TTCTCCACATCCTCGCTCATTCAAGGTATCAGTCTTTGTAAAGTCTCCTATTCTGAGGT
GAAATTCCTTTTCACTTCTGCTTCTAGTCCATTTAGTGTGCTATAGTGAATATCTGAG
ACAGGTAATTTATAAAGAAAAGACATTTATTTAGCTCACAGTCCGCGAGGCTGGGAAGT (SEQ ID NO:43)

FIGURE 3BB

- 4113 CAGTTACTTTTCGTAGGATAAATTTTGGAGGAGTGGACATTGCTGAGTCTGAAGGTAACACA
CATTTTAAACTGGGATACGTATTGCCTTTTCGGAACCTTAGACCCATTTTCACTCTTTTG
ACTGACAGTGCTTGCTTCTCCACATCCTCGCTCATTACAGGTATCAGTCTTTGTAAAGTC
TCCTATTCTGCAGGTGAAATTCCTTTTCATTTCTGTCTTAGTCCATTTAGTGTGCTAT
AGTGGAAATATCTGAGACAGGGTAATTTATAAAGAAAAGACATTTATTTAGCTCACAGTTC
[C,T]
GCAGGCTGGGAAGTTTAAGAAGCGTGGTGTGGCATCTGCTGGACTCCTGGGGAGGGCTT
TCCTGCTGTGTACAACATGGTGGAAAGTCAAAGTGGAAAGTGGACATGTGTGAAGAAGCA
AAATCCGAGGGGTGTCTGGCTTTATAGCAACCCAGCCTCGAGGGAAGTATCCATTACT
GAGGGAAGTAAATTCAGTCTCATGAGAGAGAGAACTCACTCACTACTGCAAGAATGACACC
AAGCCATTATGAGGGATCTGCCTCCGTAAACCCTGACACCTCCTGCTAGGTCCCTCCTCC (SEQ ID NO:44)
- 4337 CATTTAGTGTGCTATAGTGAATATCTGAGACAGGGTAATTTATAAAGAAAAGACATTT
ATTTAGCTCACAGTTCGCGAGGCTGGGAAGTTTAAGAAGCGTGGTGTGGCATCTGCTGG
ACTCCTGGGGAGGGCTTTCTGCTGTGTACAACATGGTGGAAAGTCAAAGTGGAAAGTGG
ACATGTGTGAAGAAGCAAAATCCGAGGGGTGTCTGGCTTTATAGCAACCCAGCCTCGAG
GGAAGTATCCATTACTGAGGGAAGTAAATTCAGTCTCATGAGAGAGAGAACTCACTCACT
[A,G]
CTGCAAGAATGACACCAAGCCATTCATGAGGGATCTGCCTCCGTAAACCCTGACACCTCCT
GCTAGGTCCCTCCTCCCAACACGGCCACATCAGGGATCAGACTTCAACATGAGTTTTTGT
GGGGACAAACAAAACGTAGCACTTGCTTTGCCTTTTGGTTCTATTACATCCTCCACAGG
ATTGCATTATGCCTACCCATTTGGTGAGGGCAGTCTTCTTTAATTGGTTTACTGATTCAA
ATGCTACCCCTCCTCCAGAGACATCCTCACAGACACACCCAGAAATCATGTTTTACCAGTT (SEQ ID NO:45)
- 4473 TTCCTGCTGTGTACAACATGGTGGAAAGTCAAAGTGGAAAGTGGACATGTGTGAAGAAGC
AAAATCCGAGGGGTGTCTGGCTTTATAGCAACCCAGCCTCGAGGGAAGTATCCATTAC
TGAGGGAAGTAAATTCAGTCTCATGAGAGAGAGAACTCACTCACTACTGCAAGAATGACAC
CAAGCCATTCATGAGGGATCTGCCTCCGTAAACCCTGACACCTCCTGCTAGGTCCCTCCTC
CCAACACGGCCACATCAGGGATCAGACTTCAACATGAGTTTTTGTGGGGACAAACAAAAC
[G,A]
TAGCACTTGCTTTGCCTTTTGGTTCTATTACATCCTCCACAGGATTGCATTATGCCTAC
CCATTTGGTGAGGGCAGTCTTCTTTAATTGGTTTACTGATTCAAATGCTACCCCTCCTCCA
GAGACATCCTCACAGACACACCCAGAAATCATGTTTTACCAGTTATCTGGGCATCCCTTA
GTCCAGACGAGTTGATACATAAAATTAACCATCACATGGGATAGAATTAGGATTACAC
AGTCAACCTTTATGGGAGAAAATTTAGAGGCATGTCAGGGGTTTATGTAATGTCAAGGA (SEQ ID NO:46)
- 6455 TGTTTATTGCATTGAGTGAATCAGGATTTCACTCCATTAAGTAATTCCTCTGTAAACAA
AGAGGGTTTCAATTTATTTTATTTTATTAATATTGCTTTTTTTTTTTTTTCTGGAGAC
AGAATCTTGCTCTATACCAAGGCTGGAGTGCAGTGGTGGCATCTCGGCTCACTGCAGCC
TCTGCTTCTGGAATCAAGCGATTCTTGTGCCTCAGCCTCCCAAGCAGCTGAGATTACAG
GCACATGCCACCACACCTGGTTAACTTTGTATTTTCTAGTAGAGATGGGATTTTGCCAT
[T,G]
TTGGTCAGGCTGGTCTTGAATTCCTGGCCTCTAGTGATCTGCCTGCCTCTGCCTCTGAAA
GTGCTAAGATTACAGGCATGAGCTACCATGGCCAGCCCATTTCTTAATATTTTAATTGT
CAGACATGTTATGGTTTCTGGCACAATATTAAGAAGACATGATATGAAATCACAGGGTGA
ATTTTAGGGCATCACACAGAAAGATTATGGTATAAGAAAAACAATGGAATTCAACTAC
ATTTCTGTCAAATGTTCTAAAAATATATAAAATCTGTATCTTTGTGTTCTCTCCTGATTT (SEQ ID NO:47)
- 6533 TTATTTTCAATTAATATTGCTTTTTTTTTTTTTTTTTCTGGAGACAGAATCTTGCTCTATCAC
CAAGGCTGGAGTGCAGTGGTGGCATCTCGGCTCACTGCAGCCTCTGCTTCTCTGGATTCAA
GCGATTCTTGTGCCTCAGCCTCCCAAGCAGCTGAGATTACAGGCACATGCCACCACACCT
GGTTAACTTTTGTATTTTCTAGTAGAGATGGGATTTTGCCATGTTGGTCAGGCTGGTCTT
GAATTCCTGGCCTCTAGTGATCTGCCTGCCTCTGCCTCTGAAAGTGCTAAGATTACAGGC
[T,G,A]
TGAGCTACCATGGCCAGCCCATTTCTTAATATTTTAATTGTGACATGTTATGGTTTC
TGGCACAATATTAAGAAGACATGATATGAAATCACAGGGTGAATTTTAGGGCATCACAA
AGAAAGATTATGGTATAAGAAAAACAATGGAATTCAACTACATTTCTGTCAAATGTTCT
AAAATATATAAAATCTGTATCTTTGTGTTCTCTCCTGATTTATATTCTAAATTTGATGT

FIGURE 3CC

TATCCTTCTCTGCAGAAATAAAGTGTCTGAAAGAATGAAAAAATGGAAGAATTCTTTAG (SEQ ID NO:48)

6919 ATGAAATCACAGGGTGAATTTTAGGGCATCACAAACAGAAAGATTATGGTATAAGAAAAAC
AATGGAATCCAACACTATTTCTGTCAAATGTTCTAAATATATAAAATCTGTATCTTT
GTGTTCTCTCCTGATTTATATTCTAAATTTGATGTTATCCTTCTCTGCAGAAATAAAGTG
TCTGAAAGAATGAAAAAATGGAAGAATTTCTTAGTAAGGTATAAAATACCCCTTTCTATC
TTTGTAGCATTCTAAGCCTTTTGTACCTTTCCAACTCCCAACATGCCATATTCCTGA
[G,C]
TAGGCCACAGCCATGTACATTGATCCCTTTATTTTCTTCTCTGCCTGAGATTTCTCTC
ATTCCCCTTCTCTGCCTGGTATATGATTGCCATTGTTAAGGCCCAACTCACCTTTA
TAATCTTCTAGCCCACTTTCTTTATCGGTATTCAGAAAAAACAAGAAGCTTCCACA
AGACAACATTCTGTAATACACTGCTTAACCTCTTTTGACCCTGCTGAGTTCAAAAATCTT
ATCTTTTAAAGGATTGAATGGAGTCCACCAAGGTATCTATTTTGACAGGATTTATGAAA (SEQ ID NO:49)

7305 GATTGCCCATGTTTAAAGGCCCAACTCACCTTTATAATCTTCTAGCCCACTTTCTTTA
TCGGTATTCAGAAAAAACAAGAAGCTTCCACAAGACAACATTCTGTAATACACTGCT
TAACTCTTTTGACCCTGCTGAGTTCAAAAATCTTATCTTTTAAAGGATTGAATGGAGTC
CACCAAGGTATCTATTTTGACAGGATTTATGAAAAACAAGGATTTGTTGAGAAAGTTT
GAAGCCTAACTCTGAAACGTGGATCATAGTGTTTACTACACATTAAGTGTTTTAGTGGAT
[G,A]
TAATAGTTATTATTATAGGCTGTGGAATCAGAACAGGGTTCAAATGTTTTACCGCTTGC
TAGACTGTGGCCTTGGGCATGTTATTTAATGCCTGGAGGCCTCAAATGTTAACTAGGAAT
GGTAAGACCTACCCAGTAACTTAGCATAAATAGTAAATTCATTCAATTAATGTTTTCAA
CAGTGCCAGACATTGTTTAACTGAACTGGGGATATAGTGGTGAACAACACTGACAGCGTTC
TTCATTGTATTCTCAAAACCTCCCTATAGTAAGTAGGTCTGTGTGTGTGTAGGTGCA (SEQ ID NO:50)

7340 TAATCTTCTAGCCCACTTTCTTTATCGGTATTCAGAAAAAACAAGAAGCTTCCACA
AGACAACATTCTGTAATACACTGCTTAACCTCTTTTGACCCTGCTGAGTTCAAAAATCTT
ATCTTTTAAAGGATTGAATGGAGTCCACCAAGGTATCTATTTTGACAGGATTTATGAAA
ACAAAAGGATTTGTTGAGAAAGTTTGAAGCCTAACTCTGAAACGTGGATCATAGTGTTA
CTACACATTAAGTGTTTTAGTGGATGTAATAGTTATTATTATAGGCTGTGGAATCAGAAC
[A,G]
GGGTTCAAATGTTTTACCGCTTGTAGACTGTGGCCTTGGGCATGTTATTTAATGCCTG
GAGGCCTCAAATGTTAACTAGGAATGGTAAGACCTACCCAGTAACTTAGCATAAATAGTA
AATTCATTCAATTAATGTTTTCAACAGTGCCAGACATTGTTTAACTGAACTGGGGATATA
GTGGTGAACAACACTGACAGCGTCTTCATTGTATTCTCAAAACCTCCCTATAGTAAGT
AGGTCTGTGTGTGTGTAGGTGCATGGGAATAAAAAATAAAGCAAATAATGAACAG (SEQ ID NO:51)

7466 TTAAGGATTGAATGGAGTCCACCAAGGTATCTATTTTGACAGGATTTATGAAAAA
GGATTTGTTGAGAAAGTTTGAAGCCTAACTCTGAAACGTGGATCATAGTGTTTACTACAC
ATTAAGTGTTTTAGTGGATGTAATAGTTATTATTATAGGCTGTGGAATCAGAACAGGGTT
CAAATGTTTTACCGCTTGTAGACTGTGGCCTTGGGCATGTTATTTAATGCCTGGAGGC
CTCAAATGTTAACTAGGAATGGTAAGACCTACCCAGTAACTTAGCATAAATAGTAAATTC
[A,G]
TTCATTTAATGTTTTCAACAGTGCCAGACATTGTTTAACTGAACTGGGGATATAGTGGTG
AACAACTGACAGCGTCTTCATTGTATTCTCAAAACCTCCCTATAGTAAGTAGGTCT
GTGTGTGTGTAGGTGCATGGGAATAAAAAATAAAGCAAATAATGAACAGGGTAAT
TTCAAAAAGCAGAAAGAGCTATTCAACAAAACCTACCTGCCTTTTATTAGATGAACTCTC
AACTCTATGGTTTGTCTCTCTCTGTCATTCTGTTAAATGCTGTGAGCCTGTTTCTTA (SEQ ID NO:52)

7589 AACTGTTTTAGTGGATGTAATAGTTATTATTATAGGCTGTGGAATCAGAACAGGGTTCAA
ATGTTTTACCGCTTGTAGACTGTGGCCTTGGGCATGTTATTTAATGCCTGGAGGCCTC
AAATGTTAACTAGGAATGGTAAGACCTACCCAGTAACTTAGCATAAATAGTAAATTCATT
CATTTAATGTTTTCAACAGTGCCAGACATTGTTTAACTGAACTGGGGATATAGTGGTGAA
CAACACTGACAGCGTCTTCATTGTATTCTCAAAACCTCCCTATAGTAAGTAGGTCTGT
[G,C]
TGTGTGTGTAGGTGCATGGGAATAAAAAATAAAGCAAATAATGAACAGGGTAATTTT
AAAAAGCAGAAAGAGCTATTCAACAAAACCTACCTGCCTTTTATTAGATGAACTCTCAAC

FIGURE 3DD

TCTATGGTTTGTCTCTCCTGTCAATTCTGTAAATGCTGTGAGCCTGTTTTCTTATCA
CCCTGGCCACGACTTCTGTCTTTCTGCTTGGTCTGTAGACTCTAACCCAAGGCTCATT
CTCTGCCTGGCTATCTGCCTTCTGTGGCTCTTGCCACTACCTACATTTCTGTGTTGCA (SEQ ID NO:53)

7810 CTGGGGATATAGTGGTGAACAACACTGACAGCGTTCTTCATTGTATTCTCAAAACCTCC
CTATAGTAAGTAGGTCTGTGTGTGTGTGTAGGTGCATGGGGAATAAAAAATAAGCAA
ATAATGAACAGGTAATTTCAAAAAGCAGAAAGAGCTATTCAACAAAACCTGCCTTT
TATTAGATGAAACTCTCAACTCTATGGTTTGTCTCTCCTGTCAATTCTGTTAAATGCTG
TCAGCCTGTTTTCTTATCACCTGGCCACGACTTCTGTCTTTCTGCTTGGTCTGTAG
[A,C]
CTCTAACCAAGGCTCATTCTCTGCCTGGCTATCTGCCTTCTGTGGCTCTTGCCACTAC
CTACATTTCTGTGTTGCACAGGGAAGGACCATTCCCTGTGGACCATAAAATTCTCTTT
TGAAAGAATTCTTCTGATTGGGCCACAGCACATCTGTGAAACAGCATTAGACATTG
CCTGCTCAGCAGCTCTGGGGGAAAATGTTTACTGAGAAGCGTACAGTAGTTTTTTGA
CTAACCATGGTGCAACCTCCTCCAGAGGGAACCTATGAGTATTTCAAGGACATGTGAT (SEQ ID NO:54)

9104 TTAACGAATTATTGTAGAAACAGAAAAACAAATACTGTGTTCTCATTTACAGGGGAGC
TAAACCTTGGGTAAATGGGCATAAAGATGGGAACAATAGACACTAGGGAATCCAAAAGG
GGGGAGGGAGGGAGGGCAAGGCTGGAAAGCTTCTACTGGGTACTTTGTTACAAAC
CTGGGTGATGGCAGATTAGGAGCTCAAACCCAGTATCACACAGTATACCTTGTAAAC
AGCTGATGGTGTAACCCCTGAATCTACAATAAAATTATTTATTTAAAAAATCATTATA
[G,A]
GGATTTTAAAAAGAAGGATTCCTAGACAGGTGCAGCCAAACAATTTTTTTAAATGTTG
GCAGGCCGCCACCGCCAGTCACTTATGCTGCAATAGCCCATGTCCCAACATTCCCAACCT
ACTTCTCTCCAAAAGAGAAGCTATACTTTAGATGGCCCTGTGCTGGGTCTCCCTGGAA
GTTTCTGGGGAAAGGGGCTTGAGTTGCCCCGACTGGACTCTTCTGGAGTGGGAGCCGG
GCTTCTGATCAGACGTGAGTGAGGCAGGAACCTCCGCGTCTCCAGCGCAGCCAGAGTG (SEQ ID NO:55)

9503 CATGTCCCAACATTCCCAACCTACTTCTCTCCAAAAGAGAAGCTATACTTTAGATGGCC
CTGTGCTGGGTTCTCCCTGGAAGTTCTGGGAAAGGGCTTGAGTTGCCCCGACTGGAC
TCTTCTGGAGTGGGAGCCGGGCTTCTGATCAGACGTGAGTGAGGCAGGAACCTCCGCG
TCTCCAGCGCAGCCAGAGTGCGGTCCACGCAGGTCCGCGTCTGCGCGCTCGCGCC
TTTGGCTGAAGCCGTTAGGATGAGCCCTCTCTTCCAGAGCTTTAACCGATGAAGGTGC
[A,T]
TTGTGTTTGGCGCCCTGAGGAGGATGCTGTCTTAGGCCTTTCCCACTGGACGTGTGTG
GTGGGCAGAGATCCGTTCTGTCGTCGACTTCCACCCGCTGGGGCTCACTCAGGCCGC
GGAGTCTCGAGGGAGACATCTCGATGGACTCCCTCTACGGAGATCTCTTTGGTACCTG
GACTATAACAAGGATGGGACCTTGGACATTTTGGAGTTTCAAGGAGGCTGGAGGATGTA
GGGGCCATTCAATCTCTAGAGGAAGCGAAGGTGGGTCTCACTGGGGCTGTAATCAGAGAG (SEQ ID NO:56)

9898 ACCCGCTGGGGCTCACTCAGGCCGCGGAGCTGCGAGGGAGACATCTCGATGGACTCCC
TCTACGGAGATCTCTTTGGTACCTGGACTATAACAAGGATGGGACCTTGGACATTTTGG
AGCTTCAGGAAGGCCTGGAGGATGTAGGGGCCATTCAATCTCTAGAGGAAGCGAAGGTGG
GTCTCACTGGGGCTGTAATCAGAGAGACGTTGGGGCTGGGAGCCCTGGAGAGGCATTGGG
CAGAGAGGGCAAAATTTACATGTTGTCAAGCTTGACCTGGGCCCACTGCAGTGTTCAAGT
[G,C]
GTTGACCAGCGTTACCGTTTATTAAGAATAACAACACAGCTAACACATTTCTCAAGTATT
TTTCTCCGTTTCTCCTTGGCTGTAGTAAAATCTCCAACCTCAGATTGCTCTCAAGATGT
TGGCTACATACAGCCTTGTCTTAGGAGTCACCTTGTTCAATGTGCTCACCTGTCATTAGT
CACCCAGAGGGGCGTCTAGGCTAAAGATGCGCCCTCCCAAGTTCAAGAACTGGAATAT
CACTTACGTGTATTTGGGAGTGGGGTGGTGATTGGAATTTCTGATGTTATGTTTTG (SEQ ID NO:57)

10196 GTGGTTGACCAGCGTTACCGTTTATTAAGAATAACAACACAGCTAACACATTTCTCAAGT
ATTTTTCTCCGTTTTCTCCTTGGCTGTAGTAAAATCTCCAACCTCAGATTGCTCTCAAGA
TGTTGGCTACATACAGCCTTGTCTTAGGAGTCACCTTGTTCAATGTGCTCACCTGTCATT
AGTCACCAGAGGGGCGTCTAGGCTAAAGATGCGCCCTCCCAAGTTCAAGAACTGGAAT
AATCACTCTACGTGTATTTGGGAGTGGGGTGGTGATTGGAATTTCTGATGTTATGTTTT
[T,C]

FIGURE 3EE

GGTTTCTGTTCTCTGGAAGGGGGCAGTGGAAGTGGCTTTTACTCTCGGGTTTCACTAGTGC
TGAGGTTTCTCATAATATGCCTTAATTGATAGACCCTAGTTATCAGTACCGAGCTTAGG
CTAACCTTCTCTTCCCCAGAAGGCTAACCTACAGGCTCCTTCTCAGCATGTTGTGCTTC
GTACATACTCCTATTGCAGTATTTCCAAGTCATTTTTCATTTGGAATTTATTATTGTATA
TAATAATTACTTTATAAGTATATTTGCTCTTTGGATGTTTGACCCGGTAGACTGGGAGAT

(SEQ ID NO:58)

12327 GTCATGTTATTTAATGCCTGGAGGCCCTCAAATGTTAACTAGGTAATGGTAAGACCTACCC
AGTAACTTAGCATAAATAGTAAATTCATTCATTTAATGTTTTCAAACAGTGCCAGACATT
GTTTAATGAACTGGGGATATAGTGGTGAACAACACTGACAGCGTCTTCATTGTATTCTC
AAAACCTCCCTATAGTAAGTAGGTCTGTGTGTGTGTGTAGGTGCATGGGGAATAAAAAA
TAATAAGCAAATAATGAACAATAAAATATTTTATTTAAAAAAGAAATGATACTTAC
[C,G,A]
TTGTCGTGTTAAGATACAAAAGCAATAACTTTTTATTGTGAAAATAGTCTGTTTTTGAAC
AATATATTGTTTTGTTTTTCTGTGAAAGTTGAGAACTAAATATACGAAGAGATAATG
GTCAGACCATAAATAAAAAAGAACTTTGACTCAAAATTTACAGCAGTCTGCCCAGAAAA
CCAGCCCTTTATCTAAAAATAACAGACCAGGAAACCAGCCTGTATGTGAGACTTATAGG
AAGTCAGGTTGCTATCTCTAGAGACAATACACAAAGCTATGCAATAACTGCTGTAAACAGC

(SEQ ID NO:59)

13749 TACAGGCGTGAGCCACCATGCGCCCAGCCATAGACTATATATTTTTGATCTGATAACTGG
TTCAGCTACTAAGTGACTAACAGGCAAGTAGCATCTATAGTGTGGATATGCTGGACAAAA
GGACATTCACCTCCTGGGCAGGATGGCAGAGAATGTTGAGAGATTTTATCATGCTACTCA
GAATGGTGTGCAATTTAAACTTATGAGTTGTTTGTCTGGAGTTTCCATTTAATAGT
TCAGACCATGGATTGACCGCAGGTAAGTGAAGTGTGGAGAGTGAACTGTGGATAAGGG
[G,A]
GGACTATTGTATTGTTAAGTCAGACTCATTAGGCAATCATAACTCTTGATTTGCCATCAG
AAATGCTGCAGAAATATGGGTTAAAAAACTGTTCAAAATAGGGTCAGGGATGTCCTT
TAAGTTGTTACTTCCAAAATGTTAGTGAAAAGTGTGGCCCCAAAGAGTGAAAGGAACAAA
TGACTAAGAGAAAATCTTGTCTTTCAGGATGACAGATTAAGAAAGCAACTTGCTGAAA
CACTGAAAATCTCTCCACTTGTAAGATAACACAAAAGTGGTAAAAGTGGTTGGAATGAA

(SEQ ID NO:60)

14150 ATAGGGTCAGGGATGTCCTTTAACTTGTTACTTCCAAAATGTTAGTGAAAAGTGTGGCCC
CAAAGAGTGAAAGGAACAAATGACTAAGAGAAAATCTTGTCTTCAGGATGACAGATTAAG
AAAGAAGCAACTTGCTGAAACACTGAAAATCTCTCCACTTGTAAGATAACACAAAAGTGG
CTAAAAGTGGTTGGAATGAATATGGCCAACTCAAGTCTGCACAGAACTAACTTGGTGATG
TTACAGCCCAAATTTCCACCACATATTTATACTAACTCCCCCGGATTTTCACACATGA
[T,C]
CTGTGAGGTAGCATGAAGAGGTAAGTATGCATGCCTAAGGACTTGGGAGACCTCCCCATT
TCCTTCCACCAATCACCCTAATCCAGAAATCCGCCCCAAACCTTTTCTAATAACTAC
CTTAAAGCCAGCATAGGGAGACAGATTTGAGCTGGACTCCTGTCTTCTGTGGGTACCT
TGCAATAAAAAGCTTTCTTTCTCAACACCTGGTATTATAGTATTGACTTCTAGTTTCT
CGGGCAGCAAGCCCCTTTGGTGGTGACTATTCTGTTCGCTGATATTTCCATTGGCCA

(SEQ ID NO:61)

14529 ACTAATCCCAGAATCCGCCCCAAACCTTTTCTAATAACTACCTTAAAGCCAGCATAGGG
AGACAGATTTGAGCTGGACTCCTGTCTTCTGTGGGTACCTTGCAATAAAAAGCTTTTCT
TTTTCTCAACACCTGGTATTATAGTATTGACTTCTAGTTTCTCGGGCAGCAAGCCCCCTT
TGGTGGTGACTATTCTGTTCGCTGATATTTCCATTGGCCAAAATATAAACCTCTTAGA
TGAAACTTCAGTACGTAATGGCGCCACAGAATGCTGTGACATTTTCTCTTGATTATA
[G,A]
CAGGTTACTTTACTGAATACCGTAGGCAGTTATAACACACTAAGTATTTGTGTATCTAAA
CATAGAAAAGATACAGTAAAAATATGGTAATTTTTTCAACTTTTGTAGTTGAGATTTGGAG
GGTATGTGCACATTTGTTACAAGGGTATATTGCATGATGCTGAGGTTTGGGGTACAATTG
AACCTGTCAACCCAGGTAGTGAGCATAGTACCAATCGATAATTTTCAACCTTGTCCA
TTCCCTCCCCGTTCTGTAGTCCCCAGTTTCTGCTTTCCCATCTTTATATCCGTGTGCA

(SEQ ID NO:62)

14653 CTCAACACCTGGTATTATAGTATTGACTTCTAGTTTCTCGGGCAGCAAGCCCCCTTTTGGT
CGGTGACTATTCTGTTCGCTGATATTTCCATTGGCCAAAATATAAACCTCTTAGATGAA
ACTTCAGTACGTAATGGCGCCACAGAATGCTGTGACATTTTCTCTTGATTATAGCAG
GTTACTTTACTGAATACCGTAGGCAGTTATAACACACTAAGTATTTGTGTATCTAAACAT

FIGURE 3FF

AGAAAAGATACAGTAAAAATATGGTAATTTTTTTCAACTTTTAGTTGAGATTTGGAGGGT.
[G,A]
TGTGCACATTTGTTACAAGGGTATATTGCATGATGCTGAGGTTTGGGGTACAATTGAACC
CTGTCACCCAGGTAGTGAGCATAGTACCCAATCGATAATTTTTCAACCCTTGCCATTCC
CTCCCCGTTCTTGTAGTCCCCAGTTCTGCTTTTCCCATCTTTATATCCGTGTGCACCCC
ATGTTTTGCTCCCATGTGTATGTGAGAACTTGTGGTGTGGTTTTCTATTTCTGCGTTG
ATTCGCTTAGGATAATGGCCTTCAGCTGCATCCATGTTGCTGCAGAGGACGTGATTTTAT (SEQ ID NO:63)

15871 AGGAGTTTATCAATTTTATTAGTCTTTTCAAAGAACCATCTTTTGGCTTTGTTAATCCTC
CCAATGGTGTGTTTTCTTTCTCATTACTTTTGGCTCTTTATTTCTTCAACTTCTTTTTT
GCTTAATTTTAAAATAATTTCTTGAGATTGAGATAAGCCTCAATGATGGGTACCGATTT
CCAGTCTTTCTTTCTTTTCTAATTATGCATTTTAAACCAGAAATCTTTCTCTAAGTGTAGC
TTTAGTTGCAGCTCACAAGTTTCAGATCTGTCTCTCAGTCTGGAGGTTGGAGATCTGACC
[A,G]
TGACCATGAAACCATCCAGTCACAATGTGGCATTATTTTTTAAATTTTTTTTTTTTTTTT
TGAGATAGAGTTTCACTCTTATTGCCTAGGCTGGTGTGCAATGGTGCGATCTCGGCTCAC
AGCAACCTCCACCTCCAGGTTCAAGCGATTCTTTGCCTCAGCCTCCCAAGTAGCTGGG
ATTACAGGCATGCGCCACCATGCCCAACTAATTTTGTATTTTATGATAGATGGGGGTTT
TCCATGTTGGTCAGGTTGGTCTTGAACCTCCCGACCTCAGGTGATCCGCCACCTCAGCCT (SEQ ID NO:64)

19244 GTGGCATTATTGGTTCATATTTTTATTTTTAGACTTCTTAATGCAAAACATATACAGT
TGATCCTCATTATTTGGGGATTCTGTATTTGCAAATTTGCCTACTCAATAAAATTTATCC
CCAAAGTAACCCCAAAATATATACTCACAGTACTTTCCAGGCATTATGGACATGCACA
GAGCAGTGAAAAACTTGAGTTGCTCAGCATGTACATTCTAGCTAGTAGAATAAGGCAAT
ACTCTGCCTTCTGTTTCAGCTCTCATACTATTAAGTCAAGTATCCCTTTCAAGGTCT
[G,A]
TTTTGTGCCAGTTTTTGCATTTTTGTATTTTGTGGTAATTTCTTTTTAAATGTTCC
CCAAAGGTAGTGCTGAAGTGCTGTCTAGTGTCTTAAGTGCAAGAAAGCCATAGCATGCC
TTATGGAGAAAAATATATGCGTTGGATAAGCTTTGCCCAAATTCATGTTAGTGAATCAA
CAGCACACATTAAATGAGGTGCCTTCAAACAGAAACAGACATAAGACATGGTTATGTATT
AATCAGTTGATGAAAGTGTGTAATCAGAGGCTCACAGGAACCTAACCCTGTTTTCTCTG (SEQ ID NO:65)

19387 CTCACAGTACTTTCCAGGCATTATGGACATGCACAGAGCAGTGAAAACTTGAGTTGC
TCAGCATGTACATTCTAGCTAGTAGAATAAGGCAATACTCTGCCTTCTTGTTCAGCTC
TCATACTATTAAGTCAAGTATCCCTTTCAAGGTCTATTTTGTGCCAGTTTTTGCAATT
TTGTATTTTTGTGGTAATTTCTTTTTAAATGTTCCCAAAGGTAGTGCTGAAGTGCT
GTCTAGTGTTCTTAAGTGCAAGAAAGCCATAGCATGCCTTATGGAGAAAATATATGCGTT
[T,G]
GATAAGCTTTGCCCCAAATTCATGTTAGTGAATCAACAGCACACATTAAATGAGGTGCC
TTCAAACAGAAACAGACATAAGACATGGTTATGTATTAATCAGTTGATGAAAGTGTGTA
ATCAGAGGCTCACAGGAACCTAACCCTGTTTTCTGTAGGAACAATGGTTGGTATTTG
CTAATTCAGTGTTTGCAATGAATATAGAACCTTATGGAAGATGATTGCTGTGAATAATGA
GAATTAACCATATCTCTTAAAGAGTGCATTTCTAAAGGAGAATATTCAGAAGGGTATTG (SEQ ID NO:66)

19447 TCAGCATGTACATTCTAGCTAGTAGAATAAGGCAATACTCTGCCTTCTTGTTCAGCTC
TCATACTATTAAGTCAAGTATCCCTTTCAAGGTCTATTTTGTGCCAGTTTTTGCAATT
TTGTATTTTTGTGGTAATTTCTTTTTAAATGTTCCCAAAGGTAGTGCTGAAGTGCT
GTCTAGTGTTCTTAAGTGCAAGAAAGCCATAGCATGCCTTATGGAGAAAATATATGCGTT
GGATAAGCTTTGCCCCAAATTCATGTTAGTGAATCAACAGCACACATTAAATGAGGTGC
[C,G]
TTCAAACAGAAACAGACATAAGACATGGTTATGTATTAATCAGTTGATGAAAGTGTGTA
ATCAGAGGCTCACAGGAACCTAACCCTGTTTTCTGTAGGAACAATGGTTGGTATTTG
CTAATTCAGTGTTTGCAATGAATATAGAACCTTATGGAAGATGATTGCTGTGAATAATGA
GAATTAACCATATCTCTTAAAGAGTGCATTTCTAAAGGAGAATATTCAGAAGGGTATTG (SEQ ID NO:67)

20076 TCTCTCAGAATCCTGTCATCTCCTCCAGGGTCTTTCTCCAAGAAAGTCTATCCTTTCAC
CACTAACAGTAATTTGGTCTTCTCTTTTCTGGAGAAAGTCAAGTGTATGCTGCTTC

FIGURE 3GG

AGCACCAGACCCTCTCTTACTTTGTTTTGTTTTATTCTTTTTTCATGTACAGTAGTCTTAG
GATTCTCATGAGCCTGTGAGCTGCTAGAAGGAAATACAGCAGTGCTTACATTTATTGCTT
CTATTTTATTTTCTATTTTCTCTTCTGTCTTCTGATTGTTCTCTTCTGTCCACAAAAC
[T,C]
GCTCTAATTTCCCTAGTATTAAAAATTTTCTGTCTTTTGTGTCTTTTATCCTTGCTCC
CTATTTTACTGCCAGATTTTATTTTATTTTATTTTATTTTGGAGTGGAGTCTCACTC
TGTCACCCAGGCTGGGGTGAGTGGCGGATCTCAGCTCACTGCAACCTCCGCCTCCAG
CTTCAAGCAATTTTCTCTTTAGCCTCCCAAGTAGCTGGGATTATGGGCACCTGCCACC
ATGCCTGGCTGATTTTCTATTTTATAGTAGAGACGGGGTTTACCATGTTGGCCCACTG (SEQ ID NO:68)

20492 CACTCTGTACCCAGGCTGGGGTGAGTGGCGGATCTCAGCTCACTGCAACCTCCGCCT
CCCAGCTTCAAGCAATTTTCTCTTTAGCCTCCCAAGTAGCTGGGATTATGGGCACCTG
CCACCATGCTGGCTGATTTTCTATTTTATAGTAGAGACGGGGTTTCACCATGTTGGCCA
CACTGCTCTCTAAGTCTGACCTCAGGTGAACCAACCCGCCTCAGCCTCCAAAAGTGCTGG
GATTGCAGGTGTGAGTCACTGTGCCTGGCCTTTTACTGCCAGATTTTAAAAGAATAGTC
[T,-]
GTGCTTTAGCTCTATTTCTCTACTTCTCTTTAACTCAGTCATATATGATGTTT
TGCATAGTAATGTCTAGTAATTTATTAATAATGTAGAAATAGGTAATTTTAAATGAAT
AGATCCTACTTTAATTGAATTTATCTTGGAGTTAGAATATCTTGATTGGATTGATTGTTT
TGCTACTTCTTAATTACATTACTTGGTAAGGCCACTTGTGAAGTCAGTCTCTTTGGAGGA
ATATTATTTATCTATAAGGCTGTTACAATTACTGAATTTTAAAAAATGTGTATTTATTTT (SEQ ID NO:69)

20868 TAGTAATTTATTAATAATGTAGAAATAGGTAATTTTAAATGAATAGATCCTACTTTAAT
TGAATTTATCTTGGAGTTAGAATATCTTGATTGGATTTTAGTTCTGCTACTTCTTAATT
ACATTACTTGGTAAGGCCACTTGTGAAGTCAGTCTCTTTGGAGGAATATTATTTATCTAT
AAGGCTGTTACAATTACTGAATTTTAAAAAATGTGTATTTATTTTAAATGATTTGTTA
CATTTTATGATTGATGTTGGGATAGGCATTTAAGCAAGTCTATAACTCACCTACATGCA
[T,C]
AATTTTGCCTTAATCAGTTTAAAGCTTTCTCTTAAATGAGAGATTTGAAATTCATAATTT
CTGTGGTTCTTATCAGTTCTGAGTTTATTTTGGCCCTTTTATTTTAAAGGAAAA
ATTGAGGCTTTCAGAAATTGTCCAGTCTCTCCAGACACTGGGTCTGACTATTCTGAACAA
CAAGCAGAGTTGATTCTTCAAAGGTAAGCTCTTATGTTGGTCAACAATTGACTTTCACT
TTAATATCCTGCATTAGAACTCTGTGTTTGAAGTGTGGCTTTAAACACCTCCCTAGTC (SEQ ID NO:70)

20941 GAGTTAGAATATCTTGATTGGATTTAGTTCTGCTACTTCTTAATTACATTACTTGGTA
AGGCCACTTGTGAAGTCAGTCTCTTTGGAGGAATATTATTTATCTATAAGGCTGTTACAA
TTACTGAATTTTAAAAAATGTGTATTTATTTTAAATGATTTGTTACATTTTATGATT
GATGTTGGGATAGGCATTTAAGCAAGTCTATAACTCACCTACATGCATAATTTGCTTA
ATCAGTTTAAAGCTTTCTCTTAAATGAGAGATTTGAAATTCATAATTTCTGTGGTTCTTA
[T,C]
CAGTTCTGAGTTTATTTTGGCCCTTTTATTTTAAAGGAAAAATTGAGGCTTCAG
AAATTGTCCAGTCTCTCCAGACACTGGGTCTGACTATTCTGAACAACAAGCAGAGTTGA
TTCTTCAAAGGTAAGCTCTTCACTGTTGGTCAACAATTGACTTTCACTTTAATATCCTGCA
TTAGAACTCTGTGTTTGAAGTGTGGCTTTAAACACCTCCCTAGTCTTCATTATGTATA
TCCAAGATCTTTTGTCTTTTTCTCCCATTCATTTTGTATGTGTACATTTATCTAAAG (SEQ ID NO:71)

21116 GTATTGATGTTGGGATAGGCATTTAAGCAAGTCTATAACTCACCTACATGCATAATTTTG
CCTTAATCAGTTTAAAGCTTTCTCTTAAATGAGAGATTTGAAATTCATAATTTCTGTGGT
TCTTATCAGTTCTGAGTTTATTTTGGCCCTTTTATTTTAAAGGAAAAATTGAGG
CTTCAGAAATTGTCCAGTCTCTCCAGACACTGGGTCTGACTATTCTGAACAACAAGCAG
AGTTGATTCTTCAAAGGTAAGCTCTTCACTGTTGGTCAACAATTGACTTTCACTTTAATAT
[C,T]
CTGCATTAGAAGTCTGTGTTTGAAGTGTGGCTTTAAACACCTCCCTAGTCTTCATTAT
GTATATCCAAGATCTTTTGTCTTTTTCTCCCATTCATTTTGTATGTGTACATTTATC
TAAAGTGTAAGAATGGGAAGTGAAGCTCAGACTGGACTCTTCTTTCAAGGCCTCAAAG
GATAGTGAATGGCAGGAAGTAAGGTTTTAACTCCATAGATGAGGAGCTGAAGAGTTTGT
GTGTTGCTTTTTCTCCATTTGATTTCTAATGTGACAGTAAACTCATTGATTCAAACATAA (SEQ ID NO:72)

FIGURE 3HH

- 21701 CATTGATTCAAACCTAAGAAGACTAGCAGATTATCACATTATTTAACCTAGATGTGACTG
GAAAAAAGGGAAATTACTAAGCTCTCCAAGCTAACAAAGAAATACCTGTTTAACTTTCA
GAAAAACAGAAATGCAATTTTGAACCTTATTGTCTGGGGCAATCAGTTTGACTATTTAAGT
CAGACTTTTATACTCTTAATGTTTTGTTTCATGGGATAGAGCAGTAATCTCTGCAGCCCA
GGTGCTCTCAAATACTCTGTTGCTATAAACACAGGGCAGGAAGTATTTTTATGATAAC
[G,A]
TAAAAACAGAAAAGGACAATTATATTGTATTAATATTGTTGTGAATATTTTCAGTCCTCAC
ATTGTCTAAAAATCTTTCTAAATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGTG
CCAACAGCATTTTCATCCTTTCTCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGGA
AGGCTCAAAGTCTCAAGGCTGAGCACGTAATGACTTTTGTAGTACTAGATGAGAAGGGC
TTTCTGAGGAAATGAAAACCTAAAACATGAAAAGAAGATAAACAGAATTTGGACAGTGA (SEQ ID NO:73)
- 21710 AAACCTAAGAAGACTAGCAGATTATCACATTATTTAACCTAGATGTGACTGGAAAAAGG
GAAATTACTAAGCTCTCCAAGCTAACAAAGAAATACCTGTTTAACTTTTCAGAAAAACAGA
AATGCAAATTTGAACCTTATTGTCTGGGGCAATCAGTTTGACTATTTAAGTCAGACTTTT
ATACTCTTAATGTTTTGTTTCATGGGATAGAGCAGTAATCTCTGCAGCCAGGTGCTCTC
AAATACTCTGTTGCTATAAACACAGGGCAGGAAGTATTTTTATGATAACGTAAAAACAG
[A,-]
AAAGGACAATTATATTGTATTAATATTGTTGTGAATATTTTCAGTCCTCACATTGTCTAA
AAATCTTTCTAAATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGTGCCAACAGCA
TTTTTCATCCTTTCTCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGGAAGGCTCAAA
GTCTCAAGGCTGAGCACGTAATGACTTTTGTAGTACTAGATGAGAAGGGCTTTCTGAG
GAAATGAAAACCTAAAACATGAAAAGAAGATAAACAGAATTTGGACAGTGAGATATAGAG (SEQ ID NO:74)
- 21826 CAGAAATGCAAATTTGAACCTTATTGTCTGGGGCAATCAGTTTGACTATTTAAGTCAGAC
TTTTATACTCTTAATGTTTTGTTTCATGGGATAGAGCAGTAATCTCTGCAGCCAGGTGC
TCTCAAATACTCTGTTGCTATAAACACAGGGCAGGAAGTATTTTTATGATAACGTAAA
ACAGAAAAGGACAATTATATTGTATTAATATTGTTGTGAATATTTTCAGTCCTCACATTG
TCTAAAAATCTTTCTAAATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGTGCCAA
[C,T]
AGCATTTTCATCCTTTCTCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGGAAGGCT
CAAAGTCTCAAGGCTGAGCACGTAATGACTTTTGTAGTACTAGATGAGAAGGGCTTTCC
TGAGGAAATGAAAACCTAAAACATGAAAAGAAGATAAACAGAATTTGGACAGTGAGATAT
AGAGCATATAATATCTGCTTCTAAAGTAATATTCTTCTAGGAAAGTGAGGGCGTTTCCC
TGGCTGTTAGGCCAGAAATCATATTCCTATATTTCTTTGATAGCTTTAGGAATAATGCA (SEQ ID NO:75)
- 21840 TGAACCTTATTGTCTGGGGCAATCAGTTTGACTATTTAAGTCAGACTTTTATACTCTTAA
TGTTTTGTTTCATGGGATAGAGCAGTAATCTCTGCAGCCAGGTGCTCTCAAATACTCTG
TTGCTATAAACACAGGGCAGGAAGTATTTTTATGATAACGTAAAACAGAAAAGGACAA
TTATATTGTATTAATATTGTTGTGAATATTTTCAGTCCTCACATTGTCTAAAAATCTTTC
TAAATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGTGCCAACAGCATTTTCATCC
[-,T]
TTCTCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGGAAGGCTCAAAGTCTCAAGGC
TGAGCACGTAATGACTTTTGTAGTACTAGATGAGAAGGGCTTTCTGAGGAAATGAAAA
CCTAAAACATGAAAAGAAGATAAACAGAATTTGGACAGTGAGATATAGAGCATATAATAT
TCTGCTTCTAAAGTAATATTCTTCTAGGAAAGTGAGGGCGTTTCCCTGGCTGTTAGGCCA
GAAATCATATTCCTATATTTCTTTGATAGCTTTAGGAATAATGCAAATTCTAAGCCCAA (SEQ ID NO:76)
- 21841 GAACCTTATTGTCTGGGGCAATCAGTTTGACTATTTAAGTCAGACTTTTATACTCTTAAT
GTTTTGTTTCATGGGATAGAGCAGTAATCTCTGCAGCCAGGTGCTCTCAAATACTCTGT
TGCTATAAACACAGGGCAGGAAGTATTTTTATGATAACGTAAAACAGAAAAGGACAAT
TATATTGTATTAATATTGTTGTGAATATTTTCAGTCCTCACATTGTCTAAAAATCTTTC
AAATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGTGCCAACAGCATTTTCATCCT
[-,C,T]
TCTCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGGAAGGCTCAAAGTCTCAAGGC
GAGCACGTAATGACTTTTGTAGTACTAGATGAGAAGGGCTTTCTGAGGAAATGAAAAC
CTAAAACATGAAAAGAAGATAAACAGAATTTGGACAGTGAGATATAGAGCATATAATATT
CTGCTTCTAAAGTAATATTCTTCTAGGAAAGTGAGGGCGTTTCCCTGGCTGTTAGGCCAG

FIGURE 3II

- AAATCATATTCCTATATTTTCTTTGATAGCTTTAGGAATAATGCAAATTCCTAAGCCCAAG (SEQ ID NO:77)
- 21843 ACCTTATTGTCTGGGGCAATCAGTTTGACTATTTAAGTCAGACTTTTATACTCTTAATGT
TTTGTTCATGGGATAGAGCAGTAATCTCTGCAGCCAGGTGCTCTCAAATACTCTGTTG
CTATAAACACAGGGCAGGAAGTATTTTATGATAACGTAAACAGAAAAGGACAATTA
TATTGTATTAATATTGTTGTGAATATTTTCAGTCCTCACATTGTCTAAAAATCTTTCTAA
ATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGTGCCAACAGCATTTTCATCCTTT
[-,C]
TCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGGAAGGCTCAAAGTCTCAAGGCTGA
GCACGTAATGACTTTTGTAGTACTAGATGAGAAGGGCTTTCTGAGGAAATGAAAACCT
AAAACATGAAAAGAAGATAAACAGAATTTGGACAGTGAGATATAGAGCATATAATATTCT
GCTTCTAAAGTAATATTCTTCTAGGAAAGTGAGGGCGTTTCCCTGGCTGTTAGGCCAGAA
ATCATATTCCTATATTTTCTTTGATAGCTTTAGGAATAATGCAAATTCCTAAGCCCAAGCT (SEQ ID NO:78)
- 22045 ATATTTTCAGTCCTCACATTGTCTAAAAATCTTTCTAAATGGCTTTGTTATTGAATTTAT
CTCATTTTATATCTGTGCCAACAGCATTTTCATCCTTTCTCTTCATAATTTCTTTTACAA
ACAGCTGCTCAAGAGGAAGGCTCAAAGTCTCAAGGCTGAGCACGTAATGACTTTTGTAG
TACTAGATGAGAAGGGCTTTCTGAGGAAATGAAAACCTAAAACATGAAAAGAAGATAAAA
CAGAATTTGGACAGTGAGATATAGAGCATATAATATTCTGCTTCTAAAGTAATATTCTTC
[C,A,T]
AGGAAAGTGAGGGCGTTTCCCTGGCTGTTAGGCCAGAAATCATATTCCTATATTTTCTTT
GATAGCTTTAGGAATAATGCAAATTCCTAAGCCCAAGCTTCAGAATAGACTAAGAAGTATT
AGCTTAGCTGCCATGACAAAATACCATAGGCTGGATGCATTAAACAATGGAAATTTAGTT
TTTCACAGGTCTGGGAGCTGGGAAGTTTAAGATGAGAGTGCCAGCATGGTTGGGTTGTAG
TGAGGGCTCTCTTTCTGGCTTGACAGATAGACCCCTTCTCACTGTATTGTCATATGCCAGA (SEQ ID NO:79)
- 22061 CATTTGTCTAAAAATCTTTCTAAATGGCTTTGTTATTGAATTTATCTCATTTTATATCTGT
GCCAACAGCATTTTCATCCTTTCTCTTCATAATTTCTTTTACAAACAGCTGCTCAAGAGG
AAGGCTCAAAGTCTCAAGGCTGAGCACGTAATGACTTTTGTAGTACTAGATGAGAAGGG
CTTTCTGAGGAAATGAAAACCTAAAACATGAAAAGAAGATAAACAGAATTTGGACAGTG
AGATATAGAGCATATAATATTCTGCTTCTAAAGTAATATTCTTCTAGGAAAGTGAGGGCG
[G,T]
TTCCCTGGCTGTTAGGCCAGAAATCATATTCCTATATTTTCTTTGATAGCTTTAGGAATA
ATGCAAATTCCTAAGCCCAAGCTTCAGAATAGACTAAGAAGTATTAGCTTAGCTGCCATGA
CAAAATACCATAGGCTGGATGCATTAAACAATGGAAATTTAGTTTTCACAGGTCTGGGA
GCTGGGAAGTTTAAGATGAGAGTGCCAGCATGGTTGGGTTGTAGTGAGGGCTCTCTTTCT
GGCTTGACAGATAGACCCCTTCTCACTGTATTGTCATATGCCAGAGAGAGAGAGAGAGA (SEQ ID NO:80)
- 22348 GAAAGTGAGGGCGTTTCCCTGGCTGTTAGGCCAGAAATCATATTCCTATATTTTCTTTGA
TAGCTTTAGGAATAATGCAAATTCCTAAGCCCAAGCTTCAGAATAGACTAAGAAGTATTAG
CTTAGCTGCCATGACAAAATACCATAGGCTGGATGCATTAAACAATGGAAATTTAGTTT
TCACAGGTCTGGGAGCTGGGAAGTTTAAGATGAGAGTGCCAGCATGGTTGGGTTGTAGTG
AGGGCTCTCTTTCTGGCTTGACAGATAGACCCCTTCTCACTGTATTGTCATATGCCAGAGA
[-,A,G]
AG
CCATAGTCCTGTTGGATCAGGGTTCCATTCTTATGACTTTATTTGACTTTACCCCCCTAA
GATGCTATCTCCAGATATAATCACAGGTGGGTTAGGGCTCAACATTTGGATTTGGGAG
GGACACAGCTCAGTCCATAGCAAAGGATAATGCAGAGGGTTGGATATTTAAAGTAGCTA
CACAAATTTTAATATAAATATTTTATGTAACCTTTTTTTTTTTTTTGGAGATGGAGTCTAG (SEQ ID NO:81)
- 22682 ATCTTTCTCTTGCTTTCTATTATAAGGCCATAGTCCTGTTGGATCAGGGTTCCATTCTTA
TGACTTTATTTGACTTTACCCCCCTAAGATGCTATCTCCAGATATAATCACAGGTGGGT
TAGGGCTCAACATTTGGATTTGGGAGGGACACAGCTCAGTCCATAGCAAAGGATAATGC
AGAGGGTTGGATATTTAAAGTAGCTACACAATTTTAAATATAAATATTTTATGGTAAC
TTTTTTTTTTTTTGGAGATGGAGTCTAGCTCTGTTGCCAGGCTGGAGCGCAATGGTGCGA
[A,G,T]
CTCAGCTCACTGCAACCTCCGCCTCCAGGTTCAAGCAATTCCTGCCTCAGCCTCCTG
AGTAGTTGGGACTATAGGCACGCGCCACCACGCCTGGCTATTTTTTTTTTATTTTACTA

FIGURE 3JJ

23448 TTCTCTTAGTATTTTTCAAGAATAATATATTATTATTAATTGTAGTCTTCATGTTGTA
TAGTGGAGCTCTTGAACCTTATTCCTCATGTCAAGCTGAAATTGTGTGTCCTTTAACACAA
ACCATACCCGACTCCCAAAGTATTCTGCTCTCTGCTTCTATGAGATTAACTTTTCTGAT.
TCCACATGAGTGAGATCATGCAGTATTTATTTGTCTTTACCTGGCTATTTTCATTTCATAT.
TGTTACAGATAACAGGATTTCTTCTTTTTTAATGGCCGAATAGTTTTCTATTGTATAT.
[A,G]
TATAGCACATTTTCTCTCTTCATGCATTGGTGGACACTTAGGTTGATTCCGTATCTTGGC
TATCGTGAATAGTGCTATAATGAACATGGGAATGCACATGGCTCTTTGACATATTGATTT.
CATTTTATATATGTGTATATATATGTATACACACACATACAGTGGTGGGATTTGC
AGGATCATATGGTAGTTCTATATTTAATTTTTAAAGGAACCTCATACTGCTTTCCATAAT
GGCTGTATTAGTTTAACTCCTCACCAACAGGGTGCAAAAGTTCCTTTTCTCTACATACT. (SEQ ID NO:84)

[illegible]

24983 TCTGATGTTTCTTACTGATTTTCTGTTGAGATGATTTGTCTATTGCTGAAGGTAGGGTGT
TGAAGTCCCCTACTATTGCTGTATTGCAGTCTCTCTCCTTTT CAGACGTATTAATGGTT
TTTATTTTATTTTATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTTGTGAGACGGAGTCTC
ACTCTGTCAACAGGCTGGAGTGCAGTGGCAGGGTCTCGGCTCACTGCAGCCCCCGTCTCA
CGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTCGCTGGGACTACAGGCGCATGCCA
[T,C]
CACGCCCAGCTAATTTTTGTATTTTTAGTAAAGACGGGGTTTCACCATGTTGGCCAGGAT
GGTCTTGATCTCTTGACTTCATGATCCACCCGCCTTGGCCTCCCAAAGTGCTGGGATTAC
AGGTGTGAGCCACCACCCCTGGCCAATGTTTGGTATTTATCTTTAGGTGCTCTGATGTTG
GGTTCATATATATTTATAAAAAACAATAGCTACATAACTTATTAAGGGATATGCAATATA
AAATATATAAATTGTGACACTGAAAATTTAAATGGGAGGAGTGGAGTAAAGTACCTTC (SEQ ID NO:86)

FIGURE 3KK

AAGTAAAGTTACTCCTGCTCTCCTTTGGTTTCTGTTTCCATGGAATATCTTTTTCCATTC
CTTCACCATCAGTCTGTGTGATTTTTACAGATGAAATGAGTCTGTGATGGGCAGCATAT
AGTTGGATCTAGTTTTTTTAAATCCACTCAGACACTGTGTTTTTGATTGGATAATTTAAT
CCATTCATGTTCAAGGTAATTATTGATAAGTAAGGACTTTGTAACCATTTTGCTTATT
GTTTCATGGTCTTTTATAGATCCTTTATTCTTTCTCCTCTCTGCTGCTTTTTTTT (SEQ ID NO:87)

26060 GGTTTTTGGTTTGTGGTTACCAAGAGGTTACAAAAACATCTTAAGAGTTATAATAGTTT
ATTTTAACTTGATAACTTAATTTTTATTGCAAAAACCCCCAAAAACAAAAAATCTACAC
TTTTACTTAATCCCCTGAAATTTTGAATTTTGTATGTCACAGTTTACCTCTTTTCATATT
GTGTATCCCTTAAATTATTGTAGCTATTATTACTTTTAAATAGTTTCTCTTCCCTACTAC
AGATGTAAGTGATTTGCATACCATCATTACAGTATTATTTGAATTTACCTGTGTACTTT
[C,T]
TTTTATCAGCCAGTTTATACTTTTCAAGTGTTTTTGTGTTACTCATTAGCATCTTTTTCT
TTCAGCTTGAGGAGCTCCTTTTACGTTTCTTATAAAATAGGTGCGGTGATGATTATCTCC
CTCAGCTATTGTTTGTCTGGGAAAGTATCTCTCCTTCATTTCTGAAGGACACTTTGCTGG
GTACATTACCCTTGGTTGGTATTTTCTCCTTGAACGCTTTAAATATATCATCCCTTTCT
CTCCTGACCTGTAGGTCTCTGCTGACCACTGTGTTTCCAACCATATTGGGACTGTCTTA (SEQ ID NO:88)

30245 ATTTTAAACCATCCATTGTTTCTGCTTCTCTAGATAACCCTGACTAATATATAATTGGTAT
GAAGTGATATCTCATGGCTTTGATTTATATTTCTTTCATGGCTAGTGACTTTTTTTGTAC
TTTTGGGATATTGTTATTATTATTATTATTACTAGTGTTTATACTTCTTCAGTAAAA
GTGTTAGAAACAATTTTAAAGGCAGAATGTGACCAGAGTTTCTGTAGTTATATAACCA
TCATGGACCTTCCCTCAAGTGCTAAGCCATTAGTGTTACTCATGTCACTCAAATGTCAG
[C,G]
TTGTTTTCTTCCATTTCACTGTCTCTTGTGTCCCAAACCTGAATTTCATGGGAAAAACAT
CTGAATGGTGCTTAATATGGTTTGGATATTTGTCCCCTCCAAATCTCATGTTGAAATATG
ACCTCCAGTGTTGGAAGTAGGACTACTTGGGTACGAGAGTGATCCTTCATTAATGGC
TTGGTAATAAGTGAACCTCTATTAGTTCATGAAAGCTGGTTGTTGATAAGAGCCTGGCATC
TCATTTCTTGTCTTCTCTCACCATCTGACACACTTGCTCACCTTTTTTCTTCAGCCA (SEQ ID NO:89)

33664 TTCCAGAGTGTAGAAGTACACTGTCCTATCCTTTCTAGGAGATCATTATAACACCAAAAG
CAGACAGTATATGAAACAGGGAAATTAGAGGCCAAGATACCTATGACTTATATGTA AAAA
TTTAAAGAAAATATTAGCAAATGAATCAGCCATTTTAAAAAATATACCACAATCAATGC
ATTCATAAGAGCAGCTTAACAAAATTTGTTAGAAGGCATTAAAGAAGACTCAGTATAGAA
AAGATGTACCTTCTCTCAAATTTGGTGATAGAGATTCAATGCCATTAAAAAAACCCACCT
[G,T]
GTTTTTTTGGGAACTTGTCAAGCTGAGTCTCAAATTTATATCAAAGAGCAAAGGCCTAA
GAATATCCAGGACATTCTGAAGAACTGTAAAGGAGCCAGGGCCTGCCCTATCAGATACC
AAGGGTTGTTATTAAAGCCATAACCAAGTCAGTGCTGTTTCTACAGAAACAGACAAGTTAA
CAAGTGAAACATAATAGAGAGCCAGAAACAGACCCATCCATATTTGGATTGTGACGT
GAAAGAAGTAGCTTTGCAAACTTTGGGAAAAGGAGAGTGTTGCAATAGATGATGCTCG (SEQ ID NO:90)

33883 TAAAGAAGACTCAGTATAGAAAAGATGTACCTTCTCTCAAATTTGGTGATAGAGATTCAA
TGCCATTAAAAAAACCCACCTGGTTTTTTTGGGAACTTGTCAAGCTGAGTCTCAAATTT
ATATCAAAGAGCAAAGGCCTAAGAATATCCAGGACATTCTGAAGAACTGTAAGGAGCCA
GGGGCCTGCCCTATCAGATACCAAGGGTTGTTATTAAGCCATAACCAAGTCAGTGCTGTT
TCTACAGAAACAGACAAGTTAAACAAGTGAAACATAATAGAGAGCCAGAAACAGACCCAT
[C,A]
CATATTTTGGATTGTGACGTGAAAGAAGTAGCTTTGCAAACTTTGGGAAAAGGAGAGT
GTGTGCAATAGATGATGCTCGTGCTCATGCAGACAAAAAGGAAATTTGGGATACCTGCCCTC
TTACCGTACACAAACACCAACCTAAACGTGAAAGTTAACTATAACAGCTTGAGGTGGTG
GGGAAGAAATATCTTTATCTCAGTGTAAGGAAGAATTTATTTTAAAAAGAAGACACAAAA
GGCCATACATAGGAATGAAAAGATTGAATTGAGCTGCATTAAAAAGATTAAATTCAGCTG (SEQ ID NO:91)

34373 TATCTTTATCTCAGTGTAAGGAAGAATTTATTTTAAAAAGAAGACACAAAAGGCCATACA
TAGGAATGAAAAGATTGAATTCAGCTGCATTAAAAAGATTAAATTCAGCTGCGTTAAAT
CAAGAGCATCTGTAAGTGGACAGCATAGAGTGAAAGACAAAGAGAAGGTATTTGCCAGC
TTATAACTGAAGGATTAGAATGAATGATATAAAGAAGTATGTAATAAGAAAAAGACAT

FIGURE 3LL

- ACAACCGGTTAGAAAAACGGGCAAAGACATGAACAGCATATTTACGTGAAGGAAACAGC
[G,A]
GTAGCAATGAACATGGTAAGAGATGCTCAACACGTTTAGTAATTTGAAGGGAAATGCAA
GTTATACCCACAGCAAGACTATCTTATCTAGGAAGTTTGTCAATACCCTAAATGTTCTGT
GGTTTTAAGCTACAGAGTTTGTAAATTCATTTATTTATTCAATAAATACTCAGTGGCAGGC
ACTGTTTTAGAAACCTTGGTTATAACTTTGAATGAAATTAATAAATCCTTGCCTTGTG
GAGGATGCTTATGTGTGGGGAGTTGGGTGGTGGGGTCAAACAACAATTACATTAATAATAG (SEQ ID NO:92)
- 34558 ACTTGAAGGATTAGAATGAATGATATAAAGAACTATGTAATAAGAAAAAGACATACAAC
CGGTTAGAAAAACGGGCAAAGACATGAACAGCATATTTACGTGAAGGAAACAGCGGTAG
CAATGAACATGGTAAGAGATGCTCAACACGTTTAGTAATTTGAAGGGAAATGCAAGTTA
TACCCACAGCAAGACTATCTTATCTAGGAAGTTTGTCAATACCCTAAATGTTCTGTGGTT
TTAAGCTACAGAGTTTGTAAATTCATTTATTTATTCAATAAATACTCAGTGGCAGGCACTG
[G,T]
TTTAGAAACCTTGGTTATAACTTTGAATGAAATTAATAAATCCTTGCCTTGTGGAGGA
TGCTTATGTGTGGGGAGTTGGGTGGTGGGGTCAAACAACAATTACATTAATAATAGAAAT
AGTGACATAAATAAACCTATAAATATTGCAACCCAGAGTTATATTATAAATGTAAGTAGT
GACTAGGACTCTCATGCAGATATACCTCTGTGCTGGGACAAATGAAAGTTTAAGTGTAAAT
TTCCCATATGCAAGTCAAAATAAAAGTGACACTAGAAAAACACAATAATGAATATCTGAA (SEQ ID NO:93)
- 43929 GGCATTTAAGTATTCTGCCATAGGGAAGTGTAAGTTGTAGGCTTTACTTTTTATAGG
TACTATATTGTCAAATAATCTCAGCACCTCATGGTTGCTAAGGATCTGTGCTCTTGT
GGTCAGATTATGTTTATCTCTGGCATAAGGCACTTAACAATATTCAATAAAGGTTACAGA
ATCTTTTTGCTTCATCTGCTTAGCATTTTATACCAGTTTGTTCACCAAACCTTTCAA
TTTTGATTGTTTCATTAATATTCTGCATACTGATGTAACCAAGTTCTATTATTGTCAA
[T,A]
CTGCTCTGAAACCTTAGGAACTCTCTGAAGGAGTTTATTTATTTTTGTTTTGTTT
TTGTTTTGTTTTGTTTTTTGAGACGGAGTCTTGCTCTGTTGCCAGGCTAGAGTGAG
TGGTGCGATCTCGGCTCTCTGAAACTCGGCCTCCGGGTTACGCCATTCTCTGCCTC
AGCCACCGGAGTAGCTGGGACTACAGGCACCCACCACTGCGCCTGGCTAATTTTTTTGT
ATTTTTAGTAGACGGGGTTTACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTT (SEQ ID NO:94)
- 44309 TTGAGACGGAGTCTTGCTCTGTTGCCAGGCTAGAGTGAGTGCGATCTCGGCTCTC
TGCAAACTCGGCCTCCGGGTTTACGCCATTCTCTGCCTCAGCCACCGGAGTAGCTGGG
ACTACAGGCACCCACCACTGCGCTGGCTAATTTTTTTGTATTTTAGTAGAGACGGGG
TTTACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTTGTAAATCCGCCCGCCTCGCC
TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTGCCCGGCCTTTTTTTTTTTTTTT
[T,-,C]
TTTATGGGCTTGTCTTCTACACTTCAGATTTGACTAAATTAATATGCATTAAATGAAGT
CAGGAGTTACATTGCCACTAGTAACAATGCCTAAGCTTACATAAAGCATTATAAAATTTG
TTGGTGATTAGTGCCCTTCTCAGCTATGAGTATAAGATAATATTATACTAGTAGTTTCAGT
GCCTAGATAAATGTACACTATGTGAAGTTTTATTACATAATTCTTACGGTATTTTTTA
AGGTAGTTGATAACAGTTGAGACTACAATTGTATCTCCATTTATTGATAGTAAATGAA (SEQ ID NO:95)
- 44997 GAATTGTAAAAATATTATTATAGAATTGTTTCTCTCAAACTATAGTAATGTAGAATAGGT
TGAAGGGGTGATGATTTGAAACAATACCTCTCCATTAGCTAAATTTATATAGAATCTAT
TGCATGTTTTAAATGATAAGTCAGATTTATAAAAAATTTTTATAAACAGTAGGAAATGA
GTTTAGGGGTATTACATACAGTTTTAATTTTTATTTACATATTTAAACATATCATGGT
ATAAATATGATGTGGATATAAATTTGAGATAAAGGAAGTATTGTTAAGAATTGATGAAC
[T,G]
AATTTCTTAAAGATGTCATCACCAGTTGGTTTTCTAGCCTTATGAAAAATGGTTGCAAT
AAAAAGATTGACTATGATAAAATGCTGCCCTTCATTTTAACTAGACCAAGAGAAAAAC
ATACTGTGAATCTATGATGAATGAAAGAAAGTTGTAACCTGTTGGTTTTGTATATTGTAA
TTACTGTTTTTTCATTTCTTGTGAAGTGTACTGTACTTTGTTTCATTGTGAGTAGACA
ACTTATAATCTATGTAACCAATTTAGTATAAATTTCTAGGGAATGAAGTTCATATT (SEQ ID NO:96)
- 46538 TGTTATACTTATGGTCAACACTTTTTATATTTGTCTGTAGATTTCTGTACAAAAAGATTC
TGACACTGTTTTAAGCCAGCATTCCTTCAGAAATGTACCAAAATCTCAAAATTTATTAGG

FIGURE 3MM

GGCAAAGCTAATGCTTTAAAGAAAAAGGAGA

[A,G]

GGGATTGGTGTGTGTTTTCTTTAGGAACAGTAGTAACTTGACTTTTAGAGAACTTGAAT
AAGCATTTATTTTTCTTTGTCTATTTTATTGTGAAGTTTATTTATTTAAAAATAAAT
GGATTTCTCTGGAATTTAGTTTCTGCAAATTTGAGGAGTTTCAAAGTCAACCTTCAGGT
TTGATACTTCTCTAGAAAGACTCACATAACTCACTGAAAGCTTATTACCCCTGGTTATGG
TTTATTACGGGGAAAAGATGCGGATGAAAATCAGTCAAGTAAAGAAGCACATAGGGCAGA

(SEQ ID NO:97)

48153

TTATATCATTCTGCTTTTATTTTTAGGTTACGGTTCAAAATCAGACAAAATGAACATAT
TTGGTGGCTTTTCGACAGATGGTAAAAGAAGGAGGTATCCGCTCGCTTTGGAGGGGAAATG
GTACAAACGTATCAAAAATGCTCCTGAGACAGCTGTTAAATTTCTGGGCATATGAACAGG
TAATTGTTATCACCCGTGGAATTTATTAACAAAGAGGAGTTAGTAAACGGATTCAATAAA
TGTTAATGTATAATGCTTTTGGGATTCTTGTTTTAATACATGATAATCTTTCACATATAC
[T,C]

CCATAAGGAGGATCACTTATAGGAGATTAGACTAAATAAAATCAGAGATTTCTCATGACC
AAGTTATGGGATTCTTAATTCATCATATTATTTATAAAGTTTTTTTTCTAAGTAGTTTCT
TTAAAGGAAGGGTAGAATTTTAGTTTTATTCTGAATCCTGAGCAGAAGCAGCACACT
AACATAAGTTTTATGAAAGTGTCACAATCTAACCTCTGGAAGGAAAACTATAAGTTGAAG
TCCTTTGTGTAATTTGACGTTGCTGTAAAATTGAGCTGAGTTTGGAGTGACACCTCCATG

(SEQ ID NO:98)

48288

AAATTGCTCCTGAGACAGCTGTTAAATTTCTGGGCATATGAACAGGTAATTGTTATCACCC
GTGGAATTTATTAACAAAGAGGAGTTAGTAAACGGATTCAATAATGTTAATGTATAATG
CTTTTGGGATTCTTGTTTTAATACATGATAATCTTTCACATATACCCCATAGGAGGATC
ACTTATAGGAGATTAGACTAAATAAAATCAGAGATTTCTCATGACCAAGTTATGGGATTC
TTAATTCATCATATTATTTATAAAGTTTTTTTTTTCTAAGTAGTTCTTAAAGGAAGGGTA
[G,T]

AATTTTAGTTTTATTCTGAATCCTGAGCAGAAGCAGCACACTAACATAAGTTTTATG
AAAGTGTCACAATCTAACCTCTGGAAGGAAAACTATAAGTTGAAGTCTTTGTGTAATTT
GACGTTGCTGTAAAATTGAGCTGAGTTTGGAGTGACACCTCCATGAAGGCAGGGCGTG
CTTCTTCCCATGTACTCCAGCACCTAGACAGAGCTTGGCATGTGATAAGTTTCAAGCGA
GTGTTGAATGAGTCAATGAATGAACAAATGCATTTACCTCTGAATCACTTCTCTGTCGGC

(SEQ ID NO:99)

48412

TGGGATTCTTGTTTTAATACATGATAATCTTTCACATATACCCCATAGGAGGATCACTT
ATAGGAGATTAGACTAAATAAAATCAGAGATTTCTCATGACCAAGTTATGGGATTCTTAA
TTCATCATATTATTTATAAAGTTTTTTTTTTCTAAGTAGTTCTTAAAGGAAGGGTAGAAT
TTTAGTTTTATTCTGAATCCTGAGCAGAAGCAGCACACTAACATAAGTTTTATGAAA
GTGTCACAATCTAACCTCTGGAAGGAAAACTATAAGTTGAAGTCTTTGTGTAATTTGAC
[G,A]

TTGCTGTAAAATTGAGCTGAGTTTGGAGTGACACCTCCATGAAGGCAGGGGCGTGGCTTC
TTCCCATGTACTCCAGCACCTAGACAGAGCTTGGCATGTGATAAGTTTCAAGCGAGTGT
TGAATGAGTCAATGAATGAACAAATGCATTTACCTCTGAATCACTTCTCTGTCGGCTTT
GTTAACTTGGATTATTTGAGCTATTGCTTCAGCCTAACTCAATGTAAAGGGGAAATACAG
AGGTAAGTTTTAGAGTTTGGGTTCTCTTTATGGTCATTAGCAGAAGTGTCTAGTTGAGCA

(SEQ ID NO:100)

48446

CATATACCCCATAGGAGGATCACTTATAGGAGATTAGACTAAATAAAATCAGAGATTTCT
TCATGACCAAGTTATGGGATTCTTAATTCATCATATTATTTATAAAGTTTTTTTTTTCTA
AGTAGTTCTTAAAGGAAGGGTAGAATTTAGTTTTATTCTGAATCCTGAGCAGAAGC
AGCACACTAACATAAGTTTTATGAAAGTGTCACAATCTAACCTCTGGAAGGAAAACTATA
AGTTGAAGTCTTTGTGTAATTTGACGTTGCTGTAAAATTGAGCTGAGTTTGGAGTGACA
[C,G]

CTCCATGAAGGCAGGGGCGTGGCTTCTTCCCATGTACTCCAGCACCTAGACAGAGCTTG
GCATGTGATAAGTTTCAAGCGAGTGTGTAATGAGTCAATGAATGAACAAATGCATTTACC
TCTGAATCACTTCTCTGTCGGCTTTTGTTAACTTGGATTATTTGAGCTATTGCTTCAGCC
TAACTCAATGTAAAGGGGAAATACAGAGGTAAGTTTTAGAGTTTGGGTTCTCTTTATGGT
CATTAGCAGAAGTGTCTAGTTGAGCAGCCACAGATTATGTTTTCCATTATTTATTCCATC

(SEQ ID NO:101)

48456

ATAAGGAGGATCACTTATAGGAGATTAGACTAAATAAAATCAGAGATTTCTCATGACCAA
GTTATGGGATTCTTAATTCATCATATTATTTATAAAGTTTTTTTTTTCTAAGTAGTTCTT

FIGURE 3NN

- AAAGGAAGGGTAGAATTTTAGTTTATTCTGAACTCTGAGCAGAAGCAGCACAATAA
CATAAGTTTTATGAAAGTGTCACAATCTAACCTCTGGAAGGAAAACTATAAGTTGAAGTC
CTTTGTGTAATTTGACGTTGCTGTAAATTTAGCTGAGTTTGGAGTGACACCTCCATGAA
[G,C]
GCAGGGGCGGTGGCTTCTTCCCATGTACTCCAGCACCTAGACAGAGCTTGGCATGTGATA
AGTTTCAAGCGAGTGTTGAATGAGTCAATGAATGAACAAATGCATTTACCTCTGAATCAC
TTCTCTGTCGGCTTTTGTAACTTGGATTATTTGAGCTATTGCTTCAGCCTAACTCAATG
TAAAGGGGAAATACAGAGGTAAGTTTTAGAGTTTGGGTCTCTTTATGGTCATTAGCAGA
ACTGTCTAGTTGAGCAGCCACAGATTATGTTTTCCATTATTTATTCCATCATTGTTTATC (SEQ ID NO:102)
- 48789 GCACCTAGACAGAGCTTGGCATGTGATAAGTTTCAAGCGAGTGTTGAATGAGTCAATGAA
TGAACAAATGCATTTACCTCTGAATCACTTCTCTGTCGGCTTTTGTAACTTGGATTATT
TGAGCTATTGCTTCAGCCTAACTCAATGTAAAGGGGAAATACAGAGGTAAGTTTTAGAGT
TTGGGTCTCTTTATGGTCATTAGCAGAACTGTCTAGTTGAGCAGCCACAGATTATGTTT
TCCATTATTTATTCCATCATTGTTTATCAAGGACTGTAAAGGGCCTTGAATTTCAACTCCC
[C,-]
CCCCCATAGTTTTTGTATTATTCATGTAGATTTTAGATTATTCTGGAGAGTGTTTTGTT
CTTGAGCAACAGAACTACTCTTGAGAAGATTACGAAGTCCAGTGGTATCCTTTTCTTTGCC
TAGGAAATAGAGAAGCAAAAAAAAAAAAAAAAAAAATTAAGAAATCTAGTCTCCAGG
ATTTTAATTAGAACCTATCCTTGGGAAGGCTATTTTCTTATATGAAGGTTTGAAGATTC
AAATCATGATTATTAAGGGCTAATGTTTGAGATACCTTAGGTTATTCTGACCACATACT (SEQ ID NO:103)
- 48859 CATTTACCTCTGAATCACTTCTCTGTCGGCTTTTGTAACTTGGATTATTTGAGCTATTG
CTTCAGCCTAACTCAATGTAAAGGGGAAATACAGAGGTAAGTTTAGAGTTTGGGTCTC
TTTATGGTCATTAGCAGAACTGTCTAGTTGAGCAGCCACAGATTATGTTTTCCATTATTT
ATTCCATCATTGTTTATCAAGGACTGTAAAGGGCCTTGAATTTCAACTCCCCCCCCCATAG
TTTTTGTATTATTCATGTAGATTTTAGATTATTCTGGAGAGTGTTTTGTTCTTGAGCAA
[G,C]
AGAATACTCTTGAGAAGATTACGAAGTCCAGTGGTATCCTTTTCTTTGCCTAGGAAATAG
AGAAGCAAAAAAAAAAAAAAAAAAAATTAAGAAATCTAGTCTCCAGGATTTTAATTA
GAACCTATCCTTGGGAAGGCTATTTTCTTATATGAAGGTTTGAAGATTCAAATCATGAT
TATTAAGGGCTAATGTTTGAGATACCTTAGGTTATTCTGACCACATACTTGGATTTTAT
GATAGGAAAGCCACAGCCTAAAATAAATAAATACTCAATGCAGTTATTTAGTATGCAAG (SEQ ID NO:104)
- 49126 GATTATTCTGGAGAGTGTTTTGTTCTTGAGCAACAGAATACTCTTGAGAAGATTACGAAG
TCCAGTGGTATCCTTTTCTTTGCCTAGGAAATAGAGAAGCAAAAAAAAAAAAAAAAAAAAA
ATTAAAGAAATCTAGTCTCCAGGATTTTAATTAGAACCTATCCTTGGGAAGGCTATTTT
CCTTATATGAAGGTTTGAAGATTCAAATCATGATTATTAAGGGCTAATGTTTGAGATACC
CTTAGGTTATTCTGACCACATACTTGGATTTTATGATAGGAAAGCCACAGCCTAAAATAA
[A,G]
TAAATACTCAATGCAGTTATTTAGTATGCAAGAAGTTTGGTATTTTGAAGAAAGTCCAT
GGGTATTGCAAGCAAATATGCACATTTTCTTTATGCCATTTGTGAGATTCTTACCTTGG
ATACCACCAACAGGCATCCTCTGCTTCTGTCCACCAAGCTCCTTCTGAGACCTCTTTA
TAGTATTGTGATTTCTGCACACTAACTTTCTTAGACATGAAGAGAAAGCTGTCTACACAG
TGTGGTGTAGTTTTCTTATGGGCTCTGGACCTATGGTGCTGTTTTCTCTCTCTGCTGA (SEQ ID NO:105)
- 49378 TGACCACATACTTGGATTTTATGATAGGAAAGCCACAGCCTAAAATAAATAAATACTCAA
TGAGTTATTTAGTATGCAAGAAGTTTGGTATTTTGAAGAAAGTCCATGGGTATTGCAA
GCAATATGCATTTTGTCTTATGCCATTTGTGAGATTCTTACCTTGGATACCACCAAC
AGGCATCCTCTGCTTCTGTCCACCAAGCTCCTTCTGAGACCTCTTTATAGTATTGTGA
TTTCTGCACACTAACTTTCTTAGACATGAAGAGAAAGCTGTCTACACAGTGTGGTGTAGT
[T,G]
TTCTTATGGGCTCTGGACCTATGGTGCTGTTTTCTCTCTCTGCTGAAGGTCCATTCT
CCCTCGGGGCTCTCTAAAGCCACCTTCTGTGACAAGCATATACTAAGCATCTCAATCA
AAGCCAGTTCTCCCCTGTCCAGCCTCCCTCGAGTGCTGAATTGCAGAAATATCCATTTT
TCATTGGATGATGGAAGCCATTGTTTTCCAGTGGATTGTAAATTAATTCGGGGTAAA
TAGGCTGTATATTTCTCAAATTTCCAGAGTATGTAAGTGGTCACTTTAGATTGAGA (SEQ ID NO:106)

FIGURE 300

- 49482 TCCATGGGTATTGCAAGCAAATATGCACATTTTGCTTTATGCCATTTGTCAGATTCTTAC
CTTGGATACCACCAACAGGCATCCTCTGCTTCTGTCCACCCAAGCTCCTTCTGAGACCT
CTTTATAGTATTGTGATTTCTGCACACTAACTTTCTTAGACATGAAGAGAAAGCTGTCTA
CACAGTGTGGTGTAGTTTCTTATGGGCTCTGGACCTATGGTGCTGTTTTCTCTCCTCCT
GCTGAAGGTCATTATCCCTCGGGGCTCTCTAAAAGCCACCTTCTGTGACAAGCATAT
[A,C]
CTAAGCATCTCAATCAAAGCCAGTTCTCTCCCTGTCCAGCCTCCCTCGAGTGCTGAATTG
CAGAATATCCCATTTTTCATTGGATGATGGAACCCATTGTTTTCCAGTGGAATTGTAA
ATTACTTCGGGGTAAATAGGCTGTATATATTCTCAAATTTCCAGAGTATGTAAGTGGT
CACTTTTAGATTAGATAGATTTTGTTCCTTGAATAGCTAGTACTTAGGAACTAAGAA
AAAGATCTTTTCAACCTGGTATGTAGCTCTGTCAAACACATCATCAGTATGGGGTAAACC (SEQ ID NO:107)
- 49741 CTCGGGGCTCTCTAAAAGCCACCTTCTGTGACAAGCATATACTAAGCATCTCAATCAA
GCCAGTTCTCTCCCTGTCCAGCCTCCCTCGAGTGCTGAATTGCAGAATATCCCATTTTTC
ATTGGATGATGGAACCCATTGTTTTCCAGTGGAATTGTAAATTAATTCGGGGTAAATA
GGCTGTATATATTCTCAAATTTCCAGAGTATGTAAGTGGTCACTTTTAGATTAGATA
GATTTTGTTCCTTGAATAGCTAGTACTTAGGAACTAAGAAAAAGATCTTTTCAACCTG
[G,A]
TATGTAGCTCTGTCAAACACATCATCAGTATGGGGTAAACCTGTGTTCTCTGTGGGTGT
CATTACCATAGTAGTGTATTGTATCATTGACAGTGAATAGTGTGGGGTAGTGTCTTG
TGGTTTCAGCTGCCACTCTGTACTGACTGCTTCCACTCCA (SEQ ID NO:108)
- 49840 ATCTTTTCAACCTGGTATGTAGCTCTGTCAAACACATCATCAGTATGGGGTAAACCTGTG
TTCTCTGTGGGTGTGATTACCATAGTAGTGTATTGTATCATTGACAGTGA
[A,G]
TAGTGTGGGGTAGTGTCTTGTGGTTTCAGCTGCCACTCTGTACTGACTGCTTCCACTC
CAACATCTTCTCTTTATCTCAACACTGTAGGTCTACCTGTGTACTGTGTGTTTCAGCAT
CTCTGCTTGCATGACCCAGGAGTGCTCCCACTCAATATGGCCACCATGCATGGTCATCT
TTCTGCTACTCCCTGTCTCCTGACCTGTCTCAGCAACACAGACAGACACCTTCTCTT
TCTATATGTATATGGTGGGAATGCCCTTAGTACTTACTCAGGAGTAGTTCCTCTGG (SEQ ID NO:109)
- 50102 CATTACCATAGTAGTGTATTGTATCATTGACAGTGAATAGTGTGGGGTAGTGTCTTG
TGGTTTCAGCTGCCACTCTGTACTGACTGCTTCCACTCCAACATCTTCTCTTTATCTC
AACACTGTAGGTCTACCTGTGTACTGTGTGTTTCAGCATCTCTGCTTGCATGACCCAGGA
GTGCTCCCACTCAATATGGCCACCATGCATGGTCATCTTCTGCTACTCCCTGTCTCCT
GACCTGTCTCAGCAACACAGACAGACACCTTCTCTTCTATATGTATATGGTGGGG
[G,A]
ATGCCCTTAGTACTTACTCAGGAGTAGTTCCTCTGGGAAGCCTTCTGTTCTAGTTTCC
TTTTGTTACAGCACTTTCACATTGAATTCTGACGTTCTCTGTACTTATCTGCTTTGTGAG
ACTGTGAGCTTCTTAGGCAGTAGTACTTGTATTCTTAGCACCTTGCCAGTGCCAGGA
AACCTTATTAAGTAAATGAAAAGACAGAACTGACAGACTGGAATTAGAGCTCAAGCTTG
CCTCAATCTCAAGCATTAAAGATGAAGGGGAGCCGGGCGTGGTGGCTCAGCCTCTAATC (SEQ ID NO:110)
- 50109 ATAGTAGTGTATTGTATCATTGACAGTGAATAGTGTGGGGTAGTGTCTTGTGGTTTC
AGCTGCCACTCTGTACTGACTGCTTCCACTCCAACATCTTCTCTTTATCTCAACACTG
TAGGTCTACCTGTGTACTGTGTGTTTCAGCATCTCTGCTTGCATGACCCAGGAGTGCTC
CCTCAATATGGCCACCATGCATGGTCATCTTCTGCTACTCCCTGTCTCCTGACCTG
CTCAGCAACACAGACAGACACCTTCTCTTCTATATGTATATGGTGGGAATGCCC
[C,G,T]
TTAGTACTTACTCAGGAGTAGTTCCTCTGGGAAGCCTTCTGTTCTAGTTTCTTTTGT
ACAGCACTTTCACATTGAATTCTGACGTTCTCTGTACTTATCTGCTTTGTGAGACTGTGA
GCTTCTTAGGCAGTAGTACTTGTATTCTTAGCACCTTGCCAGTGCCAGGAAACCTT
ATTAAGTAAATGAAAAGACAGAACTGACAGACTGGAATTAGAGCTCAAGCTTGCTCAAT
CTCAAGCCATTAAAGATGAAGGGGAGCCGGGCGTGGTGGCTCAGCCTCTAATCCAGCAC (SEQ ID NO:111)
- 50747 CCAGCCTGGGCAACGTGGCAAAACCCATTTCTACAAAAATATAAAATTAGTTGGACG
TGGGGGTGTGTGCTGTACTCAGGATGCTGAGGTGGGAGGATCACTTGAGCTCGAGAGGC
AGAGGTTGCAGTGAGCTGGGATCACACATTGCAATCTAGCCTGGGTGATAGAATGAGAC

FIGURE 3PP

CTTGTCTCAAAAAAAAAAATAAATAAATAAATAAGGGGAAGATAAGGATTGGAACAGAA
GGAGCAGCATGTGGACAGAAATGTAGGCACAAGAAGGCATCACTCACTGAAGAGACTGAA
[G,A]
GTGGTTCACTGTGCCTCAAGACTGGTGGAGTGTGTTTCCGAAAGATAATGATGAAAGAG
CTGGACAGATAAACAGGGGCCAAATGTAATAGGAGTCTGGATTTTATTCTGAATATGGTA
GGGGCTATTGTAGCATCTTATATAGGGAAGTGAATGAGTACATTACATTTAAGGAATA
TCAACCTGAAAAAAGAGTGGAGACATTGTTGGGGAGAGTGAGGTAGACTAGAGGCAGG
AGAATATTTAAATAATTGAGGTAAGAAATGATGAACACCAGTATAAGGTGATGTCTTTAA (SEQ ID NO:112)

51272 TAGACTAGAGGCAGGGAGAATATTTAAATAATTGAGGTAAGAAATGATGAACACCAGTAT
AAGGTGATGTCTTTAAGGAATGGAGAAGGGAATGAACTGAGAAATATTTTGGAAAGTAGAA
TCAACAGAACTCACTGACTGACTGGATATGGAGGTGAGAAAGAGAAGAGTCAAGAAATGAT
ATTCTAATTTCTAAGTGTAGTGCATTCAAAGAGAATACAATATCAGGTTCCATTTT
GTGCATGCTGAGTTTGAGATGTGTGGGACATGTACAGGGAGCTGTCCAGTAAGCAATTGG
[G,A]
TATATCAGCTAGCCATTAAGAGAGAGATCTTTGATAGAGAGGTTGTTGCTGAGTTGAGCC
ATTGGAATGGGCAGGATCACTCAAGAAGAGCTTATAAATGAGAAGAATTCTAGGAATAAG
TCCAAAGGGAGAAGTAAAAGAAGAACTTGCAAAGGACACTGAGAAGAAATAGCTCGAGG
GATGGAGAAAATCCAGAGAGAGGGATGGCATAGGAGTCAGTGGAAAGGAAACGGTTTCAT
GGGGGTCACTACTGAGTGTGAATATAATAAGAATATCTTTTAGGATTTCTCAACCC (SEQ ID NO:113)

52842 TCAGGGTGGTTTTGAGGGCTCAGTTAAGTCTCCTTTAGGAAGGTTGAGTTCTGTAGCCTT
GGCAAGTTACTTAAAGTCTCTGTGACTATTACCTCATCTTAAGATGGGGACTAAGCTTG
GTGACATAGTTTTACATACCAGGCACAGTGCCTGACTTTTGGCTCTGTCTGAAGTCTT
CCCTTTGTATATGGTATGTTTCGGGGAATAGGAGCCTCAAGCACTTATCCTTTAAATATT
TATCCTCCATCAGTCACTAAACGTTTACTCTGTACTTTTGATAGGTGCTGTGGGGTCCA
[G,A]
GGTATAAAAGGTACCTTCAAAGTTACTGTTAAAGTGCAGGAAGGTTTTTAAGCAAATTAT
GTTTAATGATTTTGACAATCTGACATGCAGGAAAAATTAAGGGCCTATGCAGAAGAGGA
GTTTTATTTAAACACTCTGTAGTTGAGAAACAGAGCCCTTGAAGCAGTGATCTCTGCG
GGAGGAATGTCTGGTATTTGGGAATCTCATGAAATGATAATACTTAATTTTTATCATG
AGCAGCAAAACACAGATTTGCTAGGAGAAAGTCATCGTATGTTGTTGCATTGGGCACTTT (SEQ ID NO:114)

61837 GAGGAACCTCCATGTCATTTTCCATAGTAAGTACCTTTTTGTTTTTAACATTTCTAT
CAATGTACACCAAGATTCCAATTTCTCCATGTCCTCCCCAACACCATTAAGTGGGGTGGT
GGTCTACTACTATTGCTGTGTTGCTGTTTATTCTCCTCCCTTCAGTTCGTGAAGTGTGTTGCT
TCATATATTTAGGAGCTTAATATTAGGTCCATATGAAGTTATAATTTCTTCCTGGTAAAG
TGACCCATTTATCATTATGTAATGTCCATCTTTGTCTCTGTGACAGTTGTGTCTTAAA
[A,G]
TCTATTTTGTCTGATGTAATTATGGCCACCCCTTTTCTCTTTGGGTTCCCGTTTTTATGG
AATATCTTTTCCATCCTTTCACTTTAGCTTATGTGTGTCCTTAGATCTAAAGTGAGTC
TCATAGATAAGGTATAGTTGATTCTGTATGTGTTATTCACTCAGCAATTTATATCTTTTA
GTTAGGGGATTTAATCCATTTACATTTAAAGCAGTTACTGATAGGGAAGGACTTACTGTT
GTCATTTGGCTAGCTACCTTTTATCTTTGTCTGTGGCTTTTCTGTTTTCCCTTCCTC (SEQ ID NO:115)

62018 CATATATTTAGGAGCTTAATATTAGGTCCATATGAAGTTATAATTTCTTCCTGGTAAAGT
GACCCATTTATCATTATGTAATGTCCATCTTTGTCTCTGTGACAGTTGTGTCTTAAAA
TCTATTTTGTCTGATGTAATTATGGCCACCCCTTTTCTCTTTGGGTTCCCGTTTTTATGG
AATATCTTTTCCATCCTTTCACTTTAGCTTATGTGTGTCCTTAGATCTAAAGTGAGTC
TCATAGATAAGGTATAGTTGATTCTGTATGTGTTATTCACTCAGCAATTTATATCTTTTA
[A,G]
TTAGGGGATTTAATCCATTTACATTTAAAGCAGTTACTGATAGGGAAGGACTTACTGTTG
TCATTTGGCTAGCTACCTTTTATCTTTGTCTGTGGCTTTTCTGTTTTCCCTTCCTCT
CTTCTGGCTTCTCTGTGTTTTGTGTTTTTTTTTTTTTTTGTAGTGATATGTTCTGAT
TCCCTTCTCATTTCCCTTTGTGTGCATTCTATAGATGCTATTTTGTGGTTACCATTTGCA
ACTACATAAAGCATACTAAAGTTATAGCAACTATTTTAAGCTGTTTACAACCTAACTTC (SEQ ID

NO:116)

FIGURE 3QQ

- 65562 GACTGAAATTCAGACACATGCACTCTGATTCTAACCCTCCTGTCTGCCAGCTCTGATCCA
GAACCTTTCATGACTGATACGGCTGATAGATTGTCTATGGCTGATAGACTGTCACTTCTG
ACCTAAAAGTCTGATCATTTTACATCTGTTTCAACATCTTTGCAGCCTTTCCGGTGTGAGT
TCCAAAGTGTGTAGTGGGAATTTCAAAGCCTTTAATAATCTAGCCCCACTTTGTTCACTC
TCTGTGTAATAACCACATACAACAATTGGCTGCATCTCCATAGCACATGGTACTCCTCCC
[A,G]
TTGCTTTGGTTGTGCCAGCAACACTGGTTTTTCGCTTTCTCTTCTGCTTGTGAGGTCAT
TTCCAAGGCCAGGTCTTTGTGCTTTTTCCCAAGCTTCCAGAGCTTCTTCCATACTCCC
CTTACTTCTGAGATTTAACTGTTCTCTCTTCAAGCGCTTGTCTAGTAAGAAGGAGGCAGC
AGCAGCACTGTGGGTGGTGGAAAGTGTACCAGCTTTGGAGTCAGACCATTGGATCTCAG
CCCTACCATTTTCTACTTAGATTTTTTATAGGACAAATTTCTCCATCTTTCTAAGCCTCCA (SEQ ID NO:117)
- 65780 TCTAGCCCCACTTTGTTCACTCTCTGTGTAATAACCACATACAACAATTGGCTGCATCTC
CATAGCACATGGTACTCCTCCCGTTGTCTTGGTTGTGCCAGCAACACTGGTTTTTCGCTTT
CTCTTCTGCTTGTGAGGTCACTTTCCAAGGCCAGGTCTTTGTGCTTTTTCCCAAGCTT
CCCAGAGCTTCTTCCATACTCCCCTTACTTCTGAGATTTAACTGTTCTCTCTTCAAGCGC
TTGTCTAGTAAGAAGGAGGCAGCAGCACTGTGGGTGGTGGAAAGTGTACCAGCTTT
[G,A]
GAGTCAGACCATTGGATCTCAGCCCTACCATTTTCTACTTAGATTTTTTATAGGACAAAT
TCTCCATCTTTCTAAGCCTCCAATTGCTCACTTACAAAATTGATATAACATTTACCTTGC
AAGATTGGTATGGAAGGTAATTAACCCAGTATTTAGAACATAGTAATTAATAAATAACTA
TTATTACCATCATTACTATAGTTAGGACACTCACTGTTAGGTGCTATACAAAGAGGATCA
TAAAGGGATGTTGTCTTGGGCTTCTTGAATAAATGTTGTCTTTTACTGTATTTTAGA (SEQ ID NO:118)
- 66092 TTGGATCTCAGCCCTACCATTTTCTACTTAGATTTTTTATAGGACAAATTTCTCCATCTTT
CTAAGCCTCCAATTGCTCACTTACAAAATTGATATAACATTTACCTTGAAGATTGGTAT
GGAAGGTAATTAACCCAGTATTTAGAACATAGTAATTAATAAATAACTATTATTACCATC
ATTACTATAGTTAGGACACTCACTGTTAGGTGCTATACAAAGAGGATCATAAAGGGATG
TTGTCTTGGGCTTCTTGAATAAATGTTGTCTTTTACTGTATTTTAGAATATCATTCTG
[G,A]
GTCATAATTGTTTGTGTGCATAATAATGAAACATACTTGAATATTAATTAACCTCTTTT
TTTATTTTTTAGCCATGTTAGAAGGTTCCCCACAGCTGAATATGGTTGGCCTCTTTTCGAC
GAATTATTTCAAAGAAGGAATACCAGGACTTTACAGAGGCATCACCCCAAACCTTCATGA
AGGTGCTCCCTGCTGTAGGCATCAGTTATGTGGTTTATGAAAATATGAAGCAAACCTTAG
GAGTAACCCAGAAATGATGTTGCATTTTGTCTTAGCCTGATAATTGAAACTTTCAACA (SEQ ID NO:119)
- 66617 ATGAAGCAAACCTTAGGAGTAACCCAGAAATGATGTTGCATTTTTTGTCTTAGCCTGATA
ATTGAAACTTTCAACAATCTCTGGAGTGACTTTTTCTCCTCGAATTGAAACAAGTCTATG
GCAAAAGAAGCTGCATTTTTTCAAAAAGGGAAGATGGTAACAATGGTCACTTCAAAC
TTTGGGCTAAATTATATGTACACAGAAATGTTCAAAATCATAGTTTAAATGTGTTTTGAA
AAGGCCACAAATTATACTTTATCTTTCTTAATAATCCTGCAAACTCTGCCCCTGAATC
[C,T]
GAAATCTGAAAATGTACTGGCTTGAACAAAATTTGTTTTGTGTGTTAGAGTTATAAATCA
TTAATCTTTATTTCCGGTGGTTTACGTTTATGCCAGTTCCTTTATATTTAAATTTCTGT
TTTATATATTTGAATGTCTTTATAGATTTCTTTAAATTTCTTATAGAACCATTAATAG
AAAATCATTACATTTAAATATACCTTACAGCAAAAGCATCAAATAAGTATAGGTTTA
TGTCCTTATTTTTCTTTCAGCTGAATACGAATGAGCACAGTGGTGAATTTCTGAAGGGA (SEQ ID NO:120)
- 66892 ATCCTGCAAATCTCTGCCCTGAATCCGAAATCTGAAAATGTACTGGCTTGAACAAAATTT
GTTTTGTGTGTAGAGTTATAAATCATTAATCTTTATTTCCGGTGGTTTACGTTTATGCC
AGTTCCTTTATATTTAAATTTCTGTTTTATATATTTGAATGTCTTTATAGATTTCTTT
AAATTTCTTATAGAACCATTAATAGAAAATCATTACATTTAAATATACCTTACAGCAA
AAGCATCCAAATAAGTATAGGTTTATGTCTTATTTTTCTTTCAGCTGAATACGAATGA
[G,A]
CACAGTGGTGAATTTCTGAAGGGAAGTGATGAAATTATATTTATTTCACTGGGCACTTT
TCCATTTTACCACTGTACCATTATTTGGTTCCTGGAGTTATACACTAATTTTCACTATAT
TACTGTTAAATTACCAACACAAGGCAATTTATTTGAAAGATTCCGTTTATCCTGCCATTG
CTTTGAAAAGCAGCAGGAAACGAAATCCTTTGACTTGTATCAGCTTCTGCAGAGCATCTT

FIGURE 3RR

TGTTTTCTTTGTCTTTGTTTCCTACCTTTTGAATCAGATTCCGTTTTAGTCAGGAAGA (SEQ ID NO:121)

67263 CACTGTACCATTATTTGGTTCCTGGAGTTATACACTAATTTTCAGTATATTACTGTAAAA
TTACCAACACAAGGCAATTTATTTGAAAGATTCCGTTTATCCTGCCATTGCTTTGAAAAG
CAGCAGGAAACGAAATCCTTTGACTTGTATCAGCTTCTGCAGAGCATCTTTGTTTTCTTT
TGTCCTTTGTTTCCTACCTTTTGAATCAGATTCCGTTTTAGTCAGGAAGACTTCTTGGGA
CCATTCTTAGTAACCTGAAATTTCTTTTTTAATTGCATGAAGTGGATTGATCATGAGCAA
[G,A]
TGATGTGCTTATTTCTCCCTCACTGTTGAATATCTTTGAACTTGCTGTTTTCAATATGGG
CAGCACAAAGGTGAGAGATACATATTAATAGTAGTATGTATTACTCTTATACATTAGATA
CCTATATTTAAATGAAAGGCCCAATTTGTAAACATATACATTCAATTTCTCTTGGCCCC
AAGTTTTAGGAACATGTTAGGATATAGGAGACTTAATTTATAATAATGAGAGCATTTTTT
TATTTACTAAAGCCATTTTTATAGTCAACTATCTTTCTTATTTGTGTGATTAGAACTT (SEQ ID NO:122)

67651 ATAGTAGTATGTATTACTCTTATACATTAGATACCTATATTTAAATGAAAGGCCCAATTT
GTAAACATATACATTCAATTTCTCTTGGCCCAAGTTTTAGGAACATGTTAGGATATAG
GAGACTTAATTTATAAATGAGAGCATTTTTTATTTTACTAAAGCCATTTTTATAGTC
AACTATCTTTTCTTATTTGTGTGATTAGAACTTAGAAAAATATTTACTAGTTGAAGTTAT
TATCAGTTTTTAATTTAGTTCTTAAACTCATTTCACTTCTAATAATTTCTGTTATAAATT
[G,T]
CCAGCATTTTAATGAAAATCTAATGATGTAATAGGCATTTTCTTTATTTGAACCTACCTC
TTTTATTTTCTGAACCAAGAGAAAGATGGACTGGTGTTTGTGAAACATTTTAAAAATG
TAGTTTCATTTATATTAGTTATGTTTGATAAATGTCTCAGTATTTTATAATATGATAAG
CCTGGATTCTACTTTTAGGGTTATTTGTACTTTTGAGTAATATATAAAGTGACAAATATT
AAGGTACATGATCAGCTCTTTCTATTTTTACTCGTAAAAATTATGAAATGAATAATTTT (SEQ ID NO:123)

67935 ATTTCTGTTATAAATTGCCAGCATTTTAATGAAAATCTAATGATGTAATAGGCATTTTCT
TTATTTGAACCTACCTCTTTTATTTTCTGAACCAAGAGAAAGATGGACTGGTGTTTGTG
AAACATTTTAAAAATGAGTTTCATTTATATTAGTTATGTTTGATAAATGTCTCAGTAT
TTTTATAATATGATAAGCCTGGATTCTACTTTTAGGGTTATTTGTACTTTTGAGTAATA
TATAAAGTGACAATATTAAGGTACATGATCAGCTCTTTCTATTTTTACTCGTAAAAATTA
[C,T]
GGAAATGAATAATTTTGCTAACAACTTTGAAATTTCAAACCTCTGGAAAATATGAAAATA
TTCATTGTTTATTATGAATTTAAATTTGAAGGTATGAATGTGATTTGTCTGTACATCTTG
TATCTTTTCCAAAAAATGATTCTGTATCTTTTGGAAAAAAGCCGAGAGTTGAAGATAGTA
TATTTCTGGTAGTACTGAATATTTACTTACAGTTTCTATCAAAAAATATATTTGTTTCT
AAAATTACTTGTTTTCCAGTTTTTATTTTTTTAGAGAAAAATCTTAAGTCTCAGTTTCC (SEQ ID NO:124)

69000 TTCAGAAATAACTTATCAGTTATTTCTGTAAGCTTCTTGCTTACCTGGATACCTGACAGG
TGAGATGGCTGTAGCAGACACTGGCAGTTCCCTGCCACACACCTGTCCCTGTCCACAGC
TGCACAAGGCAGCTCTGTGTGCAATTGCCAGCATCTGCTCCTCTGTTCTCAGGGAATCTT
TGTTAGAAAAATGCTGCCATATTTGTTTCTCACCTATTAGTCTTGTCTCCAGTCAAGAG
AATAAATTTATGCAAGCAGAGATTGTAATTTACAGTATTTTGTCTTTGAGCTTGGCATT
[T,G]
GTTGCATTTGTAAAAATGTGGCATGGCTTCTCATCCCCCAATAGGAACTTTGCCAGCCC
TTTTGTTCTCATGGAATTCCTTTTTTGAAGAGACCAAGGAGTAAAAATACTGTGG
AGGGAGCAACCCTCCTTTGCCATATGCTCTCATTGGGAGACATGTGGAGCAGTCTGAAGT
CATTTAGGCCACTCTCTGGGAGAGCACATCCTATGATGTTCTCCAGCCTAGCCCCCTCC
ACTGTGCTCAAGTCCAAGCTGACCAGCTTCTGACCACAGTGTAACAAAGATGATTGTC (SEQ ID NO:125)

69134 CTGTGTGCAATTGCCAGCATCTGCTCCTCTGTTCTCAGGGAATCTTTGTTAGAAAAATGC
TGCCATATTTGTTTCTCACCTATTAGTCTTGTCTCCAGTCAAGAGAATAAATTTATGCA
AGCAGAGATTGTAATTTACAGTATTTTGTCTTTGAGCTTGGCATTAGTTGCATTTGTAA
AAATGTGGCATGGCTTCTCATCCCCCAATAGGAACTTTGCCAGCCCTTTGTTTCTCATG
GAACCTCCTTTTTTGAAGAGACCAAGGAGTAAAAATACTGTGGAGGGAGCAACCCT
[C,T]
CTTTGCCATATGCTCTCATTGGGAGACATGTGGAGCAGTCTGAAGTCATTTAGGCCACTC
TCTGGGAGAGCACATCCTATGATGTTCTCCAGCCTAGCCCCCTTCCACTGTGCTCAAGTC

FIGURE 3SS

Docket No.: CL001103CON.
Serial No.: To Be Assigned
Inventors: Gennady MERKULOV et al.
Title: ISOLATED HUMAN TRANSPORTER ...

CAAGCTGACCAGCTTTCTGACCACAGTGTAACAAAGATGATTGTCAGTGGGCCCCAGAA
TCCTATACCCAGA (SEQ ID NO:126)

FIGURE 3TT